

APPROVED	10.10.1990
CLASS	SUBCLASS
DRAFTSMAN	

FIG.1A. NUCLEOTIDE SEQUENCE OF THE PIV-3 F GENE (PCR-AMPLIFIED)

AAGTCAATACCAACAACTATTAGCAGTCAATACGTGCAAGAACAAAGAGAGAGATTCAA
 TTCAGTTATGAGTTGTTGATTAATCGTCAGTATGCACGTTCTTGTTCTTCTCTAAGTT
 10 20 30 40 50 60

AAAGCTAAATAAGAGAAATCAAAACAAGGATATAGAACACCCGGAACAACAATAACAAA
 TTTCGATTTATCTCTTTAGTTTGTCTTCCCATATCTTGTTGGGCTTGTTGTTTAGTTTT
 70 80 90 100 110 120

CATCCAATCCATTTTAAACAATAATCCAAAAGAGACCCGGCAACAACAAGCACCACAAAC
 GTAGGTTAGGTAAATTTGTTTAAAGGTTTCTCTCGGCCGTTGTGTTGTTCTCGTGGTTTG
 130 140 150 160 170 180

MET PRO THR **LEU** ILE LEU LEU ILE ILE THR THR MET ILE MET ALA **SER** SER CYS GLN
 ACAATGCCAACTTTAATACTGCTAATTATTACAACAATGATTATGGCATCTTCCCTGCCAA
 TGTACGGTTGAAATTTATGACGATTAAATAATGTTGTTACTAATACCGTAGAAGGACGGTT
 190 200 210 220 230 240

ILE ASP ILE THR LYS LEU GLN HIS VAL GLY VAL LEU VAL ASN SER PRO LYS GLY MET LYS
 ATACATATCACAAACCTACAGCATGTAGGTGTTATTTGGTCAACAGTCCCAAAGGATGAAG
 TATGTATAGTGTTTGTGATGTCGTACATCCACATAACCAGTTGTCAAGGTTTCCCTACTTC
 250 260 270 280 290 300

ILE SER GLN ASN PHE GLU THR ARG TYR LEU ILE LEU SER LEU ILE PRO LYS ILE GLU ASP
 ATATCACAAACCTTCGAAACAAGATATCTAATTTTGAGCCTCATACCAAATAAGAGAC
 TATAGTGTTTGAAGCTTTGTTCTATAGATTAAAACTCGGAGTATGGTTTATTCTCTCTG
 310 320 330 340 350 360

SER ASN SER CYS GLY ASP GLN GLN ILE LYS GLN TYR LYS ARG LEU LEU ASP ARG LEU ILE
 TCTAACTCTTGTGGTGACCAACAGATCAAAACAATACAGAGGTTATTGGATAGACTGATC
 AGATTGAGAACACCACTGGTTGTCTAGTTTGTATTGTTCTCCAATAACCTATCTGACTAG
 370 380 390 400 410 420

FIG.1B. ILE PRO LEU TYR ASP GLY LEU ARG LEU GLN LYS ASP VAL ILE VAL **THR** ASN GLN GLU SER
 ATCCCTCTATATGATGGATTAAAGATTACAGAAAGATGTGATAGTAACCAATCAAGAAATCC 480
 TAGGGAGATATACTACCTAAATTCTAATGTCTTTCTACACTATCATTTGGTTAGTTCTTAGG 470

430 440 450 460
 F2-F1 CLEAVAGE SITE

ASN GLU ASN THR ASP PRO ARG THR **ARG** **SER** PHE GLY VAL ILE GLY THR ILE ALA
 AATGAAACACACTGATCCAGAACAAAGACGATCCCTTTGGAGGGGTAAATTGGAAACCATTTGCT
 TTACTTTTGTGACTAGGGTCTTTGTTCTGCTAGGAAACCTCCCCCATTAACCTTGGTAACGA 540
 490 500 510 520 530

LEU GLY VAL ALA THR SER ALA GLN ILE THR ALA VAL ALA LEU VAL GLU ALA LYS GLN
 CTGGAGTAGCAACCTCAGCACAAATTACAGCGGCAGTTGCTCTGTGTTGAAGCCAAAGCAG
 GACCCTCATCGTTGGAGTCGTGTTTAAATGTCGCCCGTCAACGAGACCAACTTCGGTTTCGTC 600
 550 560 570 580 590

ALA **LYS** SER ASP ILE GLU LYS LEU LYS GLU ALA ILE ARG ASP THR ASN LYS ALA VAL GLN
 GCAAAATCACACATCGAAACAACTCAAGAAAGCAATCAGGGACACAAACAAGCAGTGCAG
 CGTTTTAGTGTTAGCTTTTGTAGTTTCTTCGTTAGTCCCTGTGTTTGTTCGTCACGTC 660
 610 620 630 640 650

SER VAL GLN SER SER ILE GLY ASN LEU ILE VAL ALA ILE LYS SER VAL GLN ASP TYR VAL
 TCAGTTTCAGAGCTCTATAGGAAATTTAATAGTAGCAATTAAATCAGTCCCAAGATTATGTC
 AGTCAAGTCTCGAGATATCCCTTTAAATTTATCATCGTTAATTTAGTCAGGTTCTAATACAG 720
 670 680 690 700 710

ASN **ASN** GLU ILE VAL PRO SER ILE ALA ARG LEU GLY CYS GLU ALA ALA GLY LEU GLN LEU
 AACAAACGAAATCGTGCCATCGATTGCTAGACTAGGTTGTGAAGCAGCAGGACTTCAATTA
 TTGTTGCTTTAGCACCGGTAGCTAACGATCTGATCCCAACACTTCGTCGTCCTGAAGTTAAT 780
 730 740 750 760 770

GLY ILE ALA LEU THR GLN HIS TYR SER GLU LEU THR ASN ILE PHE GLY ASP ASN ILE GLY
 GGAAATTGCAATTAAACACAGCATTTACTCAGAAATTAAACAACATATTTGGTGATAACATAGGA
 CCTTAACGTAATTGTGTCGTAATGAGTCTTAATTGTTGTATAAACCACTATTGTATCCT 840
 790 800 810 820 830 840

FIG.1C.

SER LEU GLN GLU LYS GLY ILE LYS LEU GLN GLY ILE ALA SER LEU TYR ARG THR ASN ILE
 TCGTTACAAGAAAGGAAATAAATTACAAGGTATAGCATCATTTATACCGCACAAATATC
 AGCAAATGTTCTTTTCCCTTATTTTAAATGTTCCCATATCGTAGTAATATGGCGTGTTTATAG 900
 850 860 870 880 890

THR GLU ILE PHE THR THR SER THR VAL ASP LYS TYR ASP ILE TYR ASP LEU LEU PHE THR
 ACAGAAATATTCACAACATCAACAGTTGATAAATATGATATCTATGATCTATTATTATACA
 TGTCTTTATAAAGTGTGTGTAGTTGTCAACTATTTTACTATAGATACTAGATAAATAATGT 960
 910 920 930 940 950

GLU SER ILE LYS VAL ARG VAL ILE ASP VAL ASP LEU ASN ASP TYR SER ILE THR LEU GLN
 GAATCAATAAAGGTGAGAGTTATAGATGTTGATTTGAAATGATTACTCAATCACCCCTCCAA
 CTTAGTTATTTCCACTCTCAATATCTACAACCTAAACTTACTAATGAGTTAGTGGGAGGTT 1020
 970 980 990 1000 1010

VAL ARG LEU PRO LEU LEU THR ARG LEU LEU ASN THR GLN ILE TYR LYS VAL ASP SER ILE
 GTCAGACTCCCTTTATTAACTAGGCTGCTGAACTCAGATCTACAAGTAGATTCCCAT
 CAGTCTGAGGGAAATAATTGATCCGACGACTTGTGAGTCTAGATGTTTCACTCTAAGGTAT 1080
 1030 1040 1050 1060 1070

SER TYR ASN ILE GLN ASN ARG GLU TRP TYR ILE PRO LEU PRO SER HIS ILE MET THR LYS
 TCATATAATAATCCAAACACAGAGAAATGGTATATCCCTCTTCCCAGCCATATCATGACGAAA
 AGTATATTATAGGTTTGTCTCTTACCCTATAGGGAGAAAGGTCGGTATAGTACTGCTTT 1140
 1090 1100 1110 1120 1130

GLY ALA PKE LEU GLY GLY ALA ASP VAL LYS GLU CYS ILE GLU ALA PHE SER SER TYR ILE
 GGGGCAATTTCTAGGTGGAGCAGATGTCAAGGAATGTATAGAAAGCATTCAGCAGTTATATA
 CCCCATAAAGATCCACCTCGTCTACAGTTCCCTTACATATCTTCGTAAGTCGTCAATATAT 1200
 1150 1160 1170 1180 1190

CYS PRO SER ASP PRO GLY PHE VAL LEU ASN HIS GLU KET GLU SER CYS LEU SER GLY ASN
 TGGCCCTTCTGATCCAGGATTTGTACTAAACCATGAATAAGGAGCTGCTTATCAGGAAAC
 ACGGGAGAGACTAGGTCCCTAAACATGATTTGGTACTTTACCTCTCGACGAAATAGTCTTTG 1260
 1210 1220 1230 1240 1250

004070 04262460

FIG.1D. ILE SER GLN CYS PRO ARG THR THR VAL THR SER ASP ILE VAL PRO ARG TYR ALA PHE VAL
 ATATCCCAATGTCCTCAAGAACCCACGGTCACATCAGACATTTGTTCCCAAGATATGCAATTCGTC
 TATAGGGTTACAGGTTCTTGGTGCCAGTGAGTCTGTACACAGGTTCTATACGTAAGCAG 1320
 1270 1280 1290 1300 1310

ASN GLY GLY VAL ALA ASN CYS ILE THR THR THR CYS ASN GLY ILE ASP ASN
 AATGGAGGAGTGGTTGCAAACTGTATACCAACCACCTGTACATGCAACGGAATCGACAAT
 TTACCTCCTCACCAACGTTTGACATATTTGTTGGTGACATGTACGTTGCCCTTAGCTGTTA 1380
 1330 1340 1350 1360 1370

ARG ILE ASN GLN PRO PRO ASP GLN GLY VAL LYS ILE THR THR HIS LYS GLU CYS ASN THR
 AGAATCAATCAACCAACCTGTATCAAGGAGTAAATAATTATACACATAAAGAAATGTAATACA
 TCTTAGTTAGTTGGTGGAAGTTCCTCATTTTAAATATTGTTGTTATTTCTTACATTATGT 1440
 1390 1400 1410 1420 1430

ILE GLY ILE ASN GLY MET LEU PHE ASN THR ASN LYS GLY THR LEU ALA PHE TYR THR
 ATAGGTATCAACGGAATGCTGTTCATACAAATAAGAAAGAACTCTTGCAATTCCTACACA
 TATCCATAGTTGCCCTTACGACAAAGTTATGTTTATTTCTTCCCTTGAGAACGTAAGATGTGT 1500
 1450 1460 1470 1480 1490

PRO ASN ASP ILE THR LEU ASN ASN SER VAL ALA LEU ASP PRO ILE ASP ILE SER ILE GLU
 CCAATGATATAACACTAAATAATTCTGTGCACTTGATCCCAATTGACATATCAATCGAG
 GGTTTACTATATTGTGATTTTAAAGACAAACGTGAAGTAACTGATAGTTAGTCTC 1560
 1510 1520 1530 1540 1550

LEU ASN LYS ALA LYS SER ASP LEU GLU SER LYS GLU TRP ILE ARG ARG SER ASN GLN
 CTTAACAAGCCCAATCAGATCTAGAGAAATCAAAAGAAATGGATAAGAGGTCAAATCAA
 GAATTGTTTCGGTTTAGTCTAGATCTTCTTAGTTTCTTACCTATTCTTCCAGTTTAGTT 1620
 1570 1580 1590 1600 1610 1620

LYS LEU ASP SER ILE GLY ASN TRP HIS GLN SER SER THR THR ILE ILE ILE LEU ILE
 AAACCTAGATTCTATTTGGAAACTGGCATCAATCTAGCACTACAATCAATTAATTTTAATA
 TTTGATCTAAGATAACCTTTGACCGTAGTTAGATCGTGATTTAGTATTAAATAAATTAT 1680
 1630 1640 1650 1660 1670 1680

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FIG.1E

MET ILE ILE ILE LEU PHE ILE ILE ASN VAL THR ILE ILE THR ILE ALA ILE LYS TYR TYR
 ATGATCATTAATTGTTTATAATTAAATGTAACGATAATTACAATTGCAATTAAAGTATTAC
 TACTAGTAATAACAATAATTAAATTACATTGCTATTAAATGTTAACGTTAATTCATAATG 1740
 1690 1700 1710 1720 1730

ARG ILE GLN LYS ARG ASN ARG VAL ASP GLN ASN ASP LYS PRO TYR VAL LEU THR ASN LYS
 AGAATTCAAAAGAGAAATCGAGTGGATCAAAATGACAAGCCATATGTACTAACCAACAAA
 TCTTAAGTTTTCTCTTTAGCTCACCTAGTTTACTGTTTCGGTATACATGATTGTTGTTT 1800
 1750 1760 1770 1780 1790

TGACATATCTATAGATCATTAGATATTAAATTATAAAAACCTT
 ACTGTATAGATATCTAGTAATCTATAATTTTAATATTTTTTGAA 1840
 1810 1820 1830 1840

NUCLEOTIDE SEQUENCE OF THE PIV-3 F GENE. THE CDNA SEQUENCE
 IS SHOWN IN THE PLUS (MRNA) STRAND SENSE IN THE 5' TO 3'
 DIRECTION. THE SIGNAL PEPTIDE (SP) AND THE TRANSMEMBRANE (TM)
 ANCHOR DOMAIN ARE UNDERLINED. THE PREDICTED F2-F1 CLEAVAGE SITE IS
 INDICATED BY THE ARROW (↓). AMINO ACIDS DIFFERING FROM THE
 PUBLISHED PRIMARY SEQUENCE OF THE PROTEIN ENCODED BY THE PIV-3 F
 GENE ARE BOXED.

RESTRICTION MAP OF THE PIV-3 F GENE

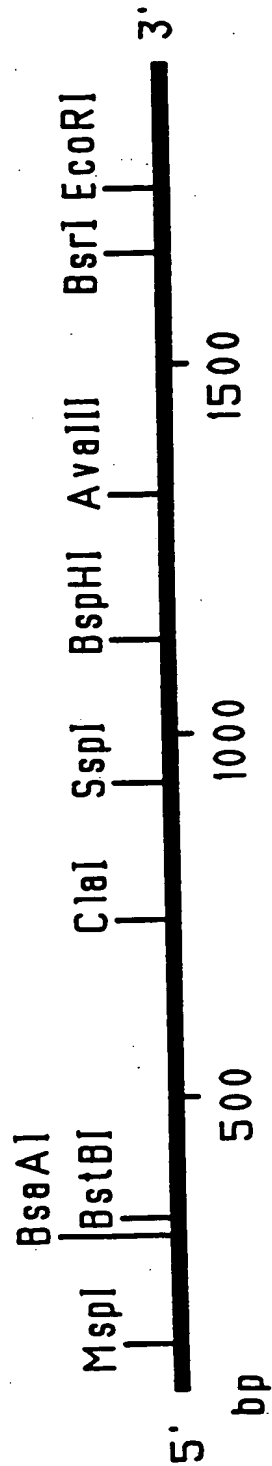


FIG.2.

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NUCLEOTIDE SEQUENCE OF THE PIV-3 HN GENE.

FIG.3A.

5' AGACAAATCCAAATTCGAGATGGAAATACCTGGAAGCATACCAATCAGGAAAGGATGCTGG
 TCTGTTTAGGTTTAAAGCTCTACCTTATGACCTTCGTATGGTTAGTGCCCTTTCCTACGACC 60
 10 20 30 40 50 60
 MET GLU TYR TRP LYS HIS THR ASN HIS GLY LYS ASP ALA GLY
 ASN GLU LEU GLU THR SER MET ALA THR [ASN] GLY ASN LYS [LEU] THR ASN LYS ILE THR TYR
 CAATGAGCTGGAGACGTCCCATGGCTACTAATGGCAACAAGCTCACCAATAAGATAACATA
 GTTACTCGACCTCTGCAAGGTACCGATGATTACCCGTTGTTTCGAGTGGTATTCTATTGTAT 120
 70 80 90 100 110 120
 ILE LEU TRP THR ILE ILE LEU VAL LEU SER ILE VAL PHE ILE ILE VAL LEU ILE ASN
 TATATTATGGACAATAATCCCTGGTGTATTATTCATAATAGTCTTCATCATAGTGCTAATTAA
 ATATAATACCTGTATTATAGGACCACCAATAAATAGTTATTCAGAAAGTAGTAGTATCAGGATTAAAT 180
 130 140 150 160 170 180
 SER ILE LYS SER GLU LYS ALA HIS GLU SER LEU LEU GLN ASP [ILE] ASN ASN GLU PHE MET
 TTCCCATCAAAAGTGAAAGGCTCATGAAATTCATTGGCTGCAAGACATAAATAATGAGTTTAT
 AAGGTAGTTTTCACCTTTTCCGAGTACTTAGTAACGACGTTCTGTATTATTACTCAATAA 240
 190 200 210 220 230 240
 GLU [ILE] THR GLU LYS ILE GLN MET ALA SER ASP ASN [THR] ASN ASP LEU ILE GLN SER GLY
 GGAAATTAACAGAAAGATCCCAAATGGCATCGGATAATACCAATGATCTAATAACAGTCAGG
 CCTTTAATGTCCTTTTCTAGGTTTACCGTAGCCCTATTATGGTTACTAGATTATGTCAGTCC 300
 250 260 270 280 290 300
 VAL ASN THR ARG LEU LEU THR ILE GLN SER HIS VAL GLN ASN TYR ILE PRO ILE SER LEU
 AGTGAATACAAAGGCTTCTTACCAATTTCAGAGTCAATGTCAGAAATTATATATACCAATATCACT
 TCACCTTATGTTCCGAAGAATGTTAAGTCTCAGTACAGGTCTTAATAATATGTTATAGTGA 360
 310 320 330 340 350 360

APPROVED	FIG.
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THR GLN GLN MET SER ASP LEU ARG LYS PHE ILE SER GLU ILE THR ILE ARG ASN ASP ASN
 GACACAACAGATGTCAGATCTTAGGAAATTCATTAGTGAATTAACAATTAGAAATGATATAA
 CTGTGTTGCTACAGTCTAGAAATCCCTTTAAGTAATCACTTTAATGTTAATCTTTACTATT
 370 380 390 400 410 420

[GLN] GLU VAL [LEU] PRO GLN ARG ILE THR HIS ASP [VAL] GLY ILE LYS PRO LEU ASN PRO ASP
 TCAAGAAAGTGCTGCCACAAGAAATAACACATGATGTGGGTATATAAACCTTTTAAATCCAGA
 AGTTCTTCACGACGGTGTTCCTTATTGTTGTTACTACACCCCATATTTTGGAATTTAGGTCT
 430 440 450 460 470 480

ASP PHE TRP ARG CYS THR SER GLY LEU PRO SER LEU MET LYS THR PRO LYS ILE ARG LEU
 TGATTTTGGAGATGACGTCCTGGTCTTCCATCTTTAATGAATACTCCAAATAAAGGTT
 ACTAAATAACCTCTACGTGCAGACCCAGAAAGGTAGAAATTTACTTTTGAGGTTTTTATTTCCAA
 490 500 510 520 530 540

MET PRO GLY PRO GLY LEU LEU ALA MET PRO THR THR VAL ASP GLY CYS [ILE] ARG THR PRO
 AATGCCAGGGCCGGGATTATTAGCTATGCTTATGCTTGTGATGGCTGTATCAGAACTCC
 TTACGGTCCCGGCCCTAAATAATCGATACGGTTGCTGACCAACTACCGACATAGTCTTGAGG
 550 560 570 580 590 600

SER LEU VAL ILE ASN ASP LEU ILE TYR ALA TYR THR SER ASN LEU ILE THR ARG GLY CYS
 GTCCCTTAGTTATAAATGATCTGATTTTATGCTTATACCTCAAACTCTAAATTAATCTCGAGGTTG
 CAGGAATCAATATTACTAGACTAAATACGAATATGGAGTTTAGATTAATGAGCTCCCAAC
 610 620 630 640 650 660

GLN ASP ILE GLY LYS SER TYR GLN VAL LEU GLN ILE GLY ILE THR VAL ASN SER ASP
 TCAGGATATAGGAAATAATCATATCAAGTCTTACAGATAGGGATATAAATGTAACCTCAGA
 AGTCCCTATATCCCTTTTAGTATAGTTTCAGAAATGTCTATCCCTATTATTGACATTTGAGTCT
 670 680 690 700 710 720

LEU VAL PRO ASP LEU ASN PRO ARG ILE SER HIS THR PHE ASN ILE ASN ASP ASN ARG LYS
 CTTGGTACCTGACTTAATAATCCAGGATCTCTCATACTTTTAAACATAAATGACCAATAGGAA
 GAACCATGGACTGAATTTAGGGTCCCTAGAGAGTATGAATAATTGTATTTACTGTTATCCTT
 730 740 750 760 770 780

FIG.38.

SRE CYS SER LEU ALA LEU LEU ASN THR ASP VAL TYR GLN LEU CYS SER THR PRO LYS VAL
 GTCATGTTCTCTAGCACTCCTAATAATACAGATGTATATCAACTGTGTTCAACTCCCAAGT
 CAGTACAAGAGATCGTGAGGATTTATGTTCTACATATAGTTGACACACAAGTTGAGGGTTTCA 840
 790 800 810 820 830

ASP GLU ARG SER ASP TYR ALA SER SER GLY ILE GLU ASP ILE VAL LEU ASP ILE VAL ASN
 TGATGAAGAATCAGATTATGCAATCATCAGGCAATAGAAAGATATTGTACTTGATTTGTCACAA
 ACTACTTTCTAGTCTAATAACGTAGTAGTCCGTATCTTCTATAACATGAACTATAACAGTT 900
 850 860 870 880 890

TYR ASP GLY SER ILE SER THR THR ARG PHE LYS ASN ASN ILE SER PHE ASP GLN PRO
 TTATGATGGCTCAATCTCAACAACAAGATTTAAGAATAATAACATAAGCTTTTGATCAACC
 AATACTACCGAGTTAGAGTTGTTCTTAAATTCTTATTATTGTTATTCGAAACTAGTTGG 960
 910 920 930 940 950

TYR ALA ALA LEU TYR PRO SER VAL GLY PRO GLY ILE TYR TYR LYS GLY LYS ILE PHE
 TTATGCTGCACCTATACCCCATCTGTGTTGGACCGGATATACTACAAAGGCAAAATAATATT
 AATACGACGTGATATGGGTAGACAACCTGGTCCCTATATGATGTTTCCGTTTATTATAA 1020
 970 980 990 1000 1010

LEU GLY TYR GLY GLY LEU GLU HIS PRO ILE ASN GLU ASN VAL ILE CYS ASN THR THR GLY
 TCTCGGGTATGGAGGTCTTGAACATCCCAATAAATGAGAAATGTAAATCTGCAACACAACCTGG
 AGAGCCCATACCTCCAGAACTTGTAGGTTTATTTACTCTTACATTAGACGTTGTGTTGACC 1080
 1030 1040 1050 1060 1070

CYS PRO GLY LYS THR GLN ARG ASP CYS ASN GLN ALA SER HIS SER PRO TRP PHE SER ASP
 GTGTCCTCCGGGAAACACAGAGAGACTGCAATCAGGCAATCTCATAGTCCATGGTTTTCAGA
 CACAGGGCCCTTTTGTGTCCTCTGACGTTAGTCCGTAGAGTATCAGGTACCAAAAGTCT 1140
 1090 1100 1110 1120 1130

ARG ARG MET VAL ASN SER ILE ILE VAL VAL ASP LYS GLY LEU ASN SER ILE PRO LYS LEU
 TAGGAGGATGGTCAACTCTATCATTTGTTGTGACAAAGGCTTAAACTCAATTCCAAATTT
 ATCCTCCTACCAAGTTGAGATAGTAACAACAACACTGTTTCCGAAATTGAGTTAAGGTTTAA 1200
 1150 1160 1170 1180 1190

FIG.3C.

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LYS VAL TRP THR ILE SER MET ARG GLN ASN TYR TRP GLY SER GLU GLY ARG LEU LEU LEU
 GAAGGTAATGGACGATATCTATATGACACAGAAATTAAGGAGGTCAGAGGAAAGGTTACTTCT
 CTTCCCATACCTGCTATAGATACTCTGCTCTTAATGACCCGCCAGTCTTCCCTTCCCAATGAAGA
 1210 1220 1230 1240 1250 1260

LEU GLY ASN LYS ILE TYR ILE TYR THR ARG SER THR SER TRP HIS SER LYS LEU GLN LEU
 ACTAGGTAAACAAGATCTATATATATACACAGATCCACAAAGTTGGCATAGCAAGTTACAAT
 TGATCCCATTTGTTCTAGATATATATATGTTCTTAGGTGTTCAACCGTATTCGTTCAATGTTAA
 1270 1280 1290 1300 1310 1320

GLY ILE ILE ASP ILE THR ASP TYR SER ASP ILE ARG ILE LYS TRP THR TRP HIS ASN VAL
 AGGAATAATTGATATTAAGGATTAAGGATTAAGGATTAAGGATTAAGGATTAAGGATTAAGGAT
 TCCCTTATTAACTATAATGACTAATGTCACCTATATTCCTATTTTACCTGTACCGTATTACA
 1330 1340 1350 1360 1370 1380

LEU SER ARG PRO GLY ASN ASN GLU CYS PRO TRP GLY HIS SER CYS PRO ASP GLY CYS ILE
 GCTATCAAGACCAAGGAACAATGAATGTTCCCATGTTCCCATGTTCCCATGTTCCCATGTTCCCAT
 CGATAGTTCTGCTCCTTTTGTACTTACAGGTACCCCTGTTAAGTACAGGTTACCTACCATACATA
 1390 1400 1410 1420 1430 1440

THR GLY VAL TYR THR ASP ALA TYR PRO LEU ASN PRO THR GLY SER ILE VAL SER SER VAL
 AACAGGAGTATATACTGATGCAATATCCACTCAATCCACACAGGGAGGCATTTGTGTCATCTGT
 TTGTCCTCATATATGACTACGTTACGTTATAGGTGAGTTAGGGTGTCCCTCGTTAACACAGTAGACA
 1450 1460 1470 1480 1490 1500

ILE LEU ASP SER GLN LYS SER ARG VAL ASN PRO VAL ILE THR TYR SER THR [ALA] THR GLU
 CATATTAGATTTCACAAATAATCGAGAGTGAACCCAGTCAATTAACCTTAACCTCAACAGCAACCGA
 GTATAATCTAAGTGTTTITAGCTCTCAGTTGAGTCAATGAAATGAGTTGTCGTTGGCT
 1510 1520 1530 1540 1550 1560

ARG VAL ASN GLU LEU ALA ILE [ARG] ASN ARG THR LEU SER ALA GLY TYR THR THR SER
 AAGAGTAAACGAGCTGGCCCATCCGAACAAGAACACTCTCAGCTGGATATACAAACAACAAG
 TTCTCATTTGCTCGACCGGTAGGCTTTTGTCTTTGTGAGAGTCGACCTATATGTTGTTGTTTC
 1570 1580 1590 1600 1610 1620

FIG.3D.

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CYS ILE THR HIS TYR ASN LYS GLY TYR CYS PHE HIS ILE VAL GLU ILE ASN GLN LYS SER
 CTGCATCACACACTATAACAAGGATATTGTTTTCATATAGTAGAATAAATCAGAAAAAG
 GACGTAGTGTGATATTGTTTCCCTATAACAAGTATATCATCTTTATTAGTCTTTTC 1680
 1630 1640 1650 1660 1670

LEU ASN THR LEU GLN PRO MET LEU PHE LYS THR GLU VAL PRO LYS SER CYS SER ***
 CTTAAACACACTTCAACCCCATGTTGTTCAAGACAGAGGTTCCAAAAGCTGCAGTTAATC
 GAATTTGTTGTAAGTTGGGTACAACAAGTTCTGCTCCAAAGGTTTTCGACGTCAAATTAG 1740
 1690 1700 1710 1720 1730

ATAATTAAACCGCAATATGCATTAAACCTATCTATATAACAAGTATATGATAAGTAATCAGC
 TATTAAATTGGCGTTATACGTAATTGGATAGATATTATGTTTCATATACCTATTATTAGTCG 1800
 1750 1760 1770 1780 1790

AATCAGACAATAGACAACAAGGGAATAATAAAAA
 TTAGTCTGTTATCTGTTTCCCTTTTATATTTT 1830
 1810

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 IS SHOWN IN THE PLUS (MRNA) STRAND SENSE IN THE 5' TO 3'
 DIRECTION. THE TRANSMEMBRANE (TM) ANCHOR DOMAIN IS UNDERLINED. AMINO ACIDS
 DIFFERING FROM THE PUBLISHED PRIMARY SEQUENCE OF THE PROTEIN ENCODED BY THE PIV-3
 HN GENE ARE BOXED.

FIG.3E.

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BY	PLANS	SUBCLASS
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RESTRICTION MAP OF THE PIV-3 HN GENE

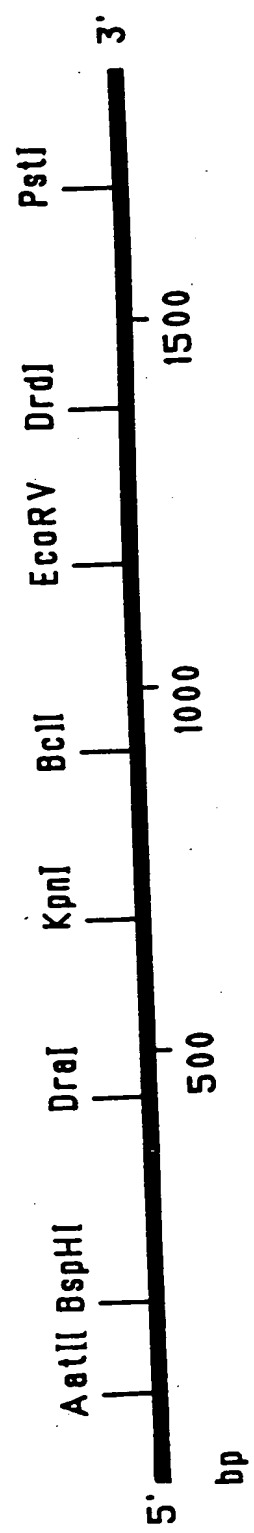


FIG.4.

NUCLEOTIDE SEQUENCE OF THE RSV F GENE.

FIG. 5A.

5' MET GLU LEU **PRO** ILE LEU LYS ALA ASN ALA ILE THR THR ILE LEU ALA **ALA** VAL THR PHE
 ATGGAGTTGGCCCAATCCCTCAAGCAAAATGCAATACCAACAATCCCTCGCTGCGAGTCACATTT
 TACCTCAACGGTTAGGAGTTTCGTTTACGTTAATGGTGTAGGAGCGACGTCAGTGTA
 10 20 30 40 50 60
 CYS PHE ALA **SER** SER GLN ASN ILE THR GLU GLU PHE TYR GLN SER THR CYS SER ALA VAL
 TGCCTTTGCTTCTAGTCAAAACATCACTGAAGAAATTTTATCAATCAACATGCGAGTGCAGTT
 ACGAAACGAAGATCAGTTTGTAGTGAATCTTAAATAGTTAGTTGACGTCACGTCACAA
 70 80 90 100 110 120
 SER LYS GLY TYR LEU SER ALA LEU ARG THR GLY TRP TYR THR SER VAL ILE THR ILE GLU
 AGCAAAAGGCTATCTTAGTGCTCTAAGAACTGGTGGTATACCTAGTGTATATACTATAGAA
 TCGTTTCCGATAGAAATCACGAGATTCTTGACCAACCAATATGATCACAATATTGATATCTT
 130 140 150 160 170 180
 LEU SER ASN ILE LYS GLU ASN LYS CYS THR ASP ALA LYS VAL LYS LEU **MET** LYS
 TTAAGTAATATCAAGGAAATAAGTGTAATGGAAACAGATGCTAAGGTAATAATTGATGAAA
 AATTCAATTATAGTTCCCTTTTATTTACATTTACCTTGCTACGATTCCCAATTTTAACTACTTT
 190 200 210 220 230 240
 GLN GLU LEU ASP LYS TYR LYS ASN ALA VAL THR GLU LEU GLN LEU MET GLN SER THR
 CAAGGAATTAGATAAATAAATAATGCTGTAAACAGAAATGCGAGTTGCTCATGCAAGCACA
 GTTCTTAATCTATTATAATTTTACGACATTGCTTAACGTCACGAGTACGTTTCGTGT
 250 260 270 280 290 300
PRO **ALA** **ALA** ASN ASN ARG ALA ARG ARG GLU LEU PRO ARG PHE MET ASN TYR THR LEU ASN
 CCAAGCAGCAAAACCAATCGAGGCCAGAGAGAACTACCAAGGTTTATGAAATATACACTCAAC
 GGTCGTCGTTTGTAGCTCGGCTCTCTCTGATGGTTCCAAATACCTTAATAATGATGAGTTG
 310 320 330 340 350 360

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ASN [THR] LYS LYS THR ASN VAL THR LEU SER LYS LYS ARG LYS ARG ARG PHE LEU GLY PHE
 AATACCAAAACCAATGTAACATTAAGCAAGAAAGGAAAGAAAGATTCTTCTTGGTTTT
 TTATGGTTTTTTTGGTTACATTTGTAATTCGTTCTTTTCTTCTTCTTAAAGAACCCAAA
 370 380 390 400 410 420

F2-F1 CLEAVAGE SITE

LEU LEU GLY VAL GLY SER ALA ILE ALA SER GLY [ILE] ALA VAL SER LYS VAL LEU HIS LEU
 TTGTTAGGTGTTGGATCTGCAATCGCCAGTGGCATTGCTGTATCTAAGGTCCCTGCACCTTA
 AACAAATCCACAACCTAGACGTTAGCGGTCACCGTTAACGACATAGATTCCAGGACGTGAAT
 430 440 450 460 470 480

GLU GLY GLU VAL ASN LYS ILE LYS SER ALA LEU LEU SER THR ASN LYS ALA VAL VAL SER
 GAAGGAGAAAGTGAAACAAGATCAAAAGTGCTCTACTATCCACAACAAGCCGCTAGTCAAGT
 CTTCCCTCTTCACTTGTTCTAGTTTTCACCGAGATGATAGGTGTTTGTTCGCGCATCAGTCA
 490 500 510 520 530 540

LEU SER ASN GLY VAL SER VAL LEU THR SER LYS VAL LEU ASP LEU LYS ASN TYR ILE ASP
 TTATCAAAATGGAGTTAGTGTTCTTAACCAAGCAAGTGTTAGACCTCAAAACTATATAGAT
 AATAGTTTACCCTCAATCACAGAAATTGGTCTGTTTTCACAATCTGGAGTTTGTGATATATCTA
 550 560 570 580 590 600

LYS GLN LEU LEU PRO ILE VAL ASN LYS ARG SER CYS [ARG] ILE SER ASN ILE GLU THR VAL
 AAACAAATTGTTACCTATTGTGAATAAGCGAAGCTGCGAGAAATATCAAAATATAGAAACTGTG
 TTTGTTAACAAATGGATAACACTTATTTCGCTTCGACGTCCTTATAGTTTATATCTTTGACAC
 610 620 630 640 650 660

ILE GLU PHE GLN HIS LYS ASN ASN ARG LEU LEU GLU ILE THR ARG GLU PHE SER VAL ASN
 ATAGAGTTCCACAACAAGAAACAACAGACTACTAGAGATTACCAAGGGAATTTAGTGTAAAT
 TATCTCAAGGTTGTGTTCTTGTCTGATGATCTCTAATGATGTTTAAATCACAATTA
 670 680 690 700 710 720

ALA GLY VAL THR THR PRO VAL SER THR TYR MET LEU THR ASN SER GLU LEU SER LEU
 GCAGGTGTAACCTACACCTGTGTAAGCACCTTACATGTTAACTAATAGTGAATTTATGTCATTA
 CGTCCACATTTGATGTGGACATTCGTGAATGTACAATTGATTTATCACTTAAATAACAGTAAT
 730 740 750 760 770 780

FIG. 5B.

ILE ASN ASP MET PRO ILE THR ASN ASP GLN LYS LYS LEU MET SER ASN ASN VAL GLN ILE
 ATCAATGATATGCCCTATAACAAATGATCAGAAAGTTAATGTTCCCAACAATGTTCAAATA
 TAGTTACTATACGGGATATTTGTTTACTAGTCTTTTCAATTTACAGGTTTACAAAGTTTAT 840
 790 800 810 820 830

VAL ARG GLN GLN SER TYR SER ILE MET SER ILE LYS GLU VAL LEU ALA TYR VAL
 GTTAGACAGCAAGTTACTCTATCATGTTCCATAATAAAGAGGAAAGTCTTAGCATATGTA
 CAACTCTGTCGTTTCAATGAGATAGTACAGGTTATTTTCTCCTTCAGGAATCGTATACAT 900
 850 860 870 880 890

VAL GLN LEU PRO LEU TYR GLY VAL ILE ASP THR PRO CYS TRP LYS LEU HIS THR SER PRO
 GTACAAATTACCACCTATATGGTGTGATAGATACACCTTGTGGAAATTACACACATCCCT
 CATGTTAAATGGTGATATACCCACACTATCTATGTGGAACAACCTTTAAATGTTGTAGGGGA 960
 910 920 930 940 950

LEU CYS THR THR ASN THR LYS GLU GLY SER ASN ILE CYS LEU THR ARG THR ASP ARG GLY
 CTATGTACAACCAACACAACAAAGAGGAGGTTCAACATCTGTGTTTAAACAAGAACTGACAGAGGA
 GATACATGTTGGTGTGTTTCTTCCCAAGTTTGTAGACAATAATGTTCTTGGACTGTCCT 1020
 970 980 990 1000 1010

TRP TYR CYS ASP ASN ALA GLY SER VAL SER PHE PHE PRO GLN ALA GLU THR CYS LYS VAL
 TGGTACTGTGACAAATGCGAGGATCAGTATCTTTCTTCCCAACAAGCTGAAACAATGTAAGTT
 ACCATGACACACTGTACGTCCTAGTCATAGAAAGAGGAGGTTTCGACTTTGTACATTTCAA 1080
 1030 1040 1050 1060 1070

GLN SER ASN ARG VAL PHE CYS ASP THR MET ASN SER LEU THR LEU PRO SER GLU VAL ASN
 CAATCGAATCGAGTATTTTGTGACACAATGAAACAGTTTAAACATTAACCAAGTGAAGTAAAT
 GTTAGCTTAGCTCATAAACACACTGTGTACTTGTCAAAATTTGTAATGGTTCACTTCATTTA 1140
 1090 1100 1110 1120 1130

LEU CYS ASN VAL ASP ILE PHE ASN PRO LYS TYR ASP CYS LYS ILE MET THR SER LYS THR
 CTCTGCAATGTTGACATATTCAATCCCAAAATATGATTTGTAATAATATGACTTCAAAACA
 GAGACGTTACAACCTGTATAAAGTTAGGGTTTATACTAACATTTTAAATACCTGAAGTTTGT 1200
 1150 1160 1170 1180 1190

FIG.5C.

ASP VAL SER SER SER VAL ILE THR SER LEU GLY ALA ILE VAL SER CYS TYR GLY LYS THR
GATGTAAAGCAGCTCCGTTATCACATCTCTAGGAGCCCATTTGTGTCATGCTATGGCAAACT
CTACATTTCGTCGAGGCAATAGTGTAAGAGATCCCTCGGTAAACACAGTACCGATACCGTTTGA
1210 1220 1230 1240 1250 1260

LYS	CYS	THR	ALA	SER	ASN	LYS	ASN	ARG	GLY	ILE	ILE	LYS	THR	PHE	SER	ASN	GLY	CYS	ASP
AAATG	TAC	AGCA	TCC	AA	TAA	AAAT	CGT	GGA	ATC	AT	AA	AG	ACA	TTT	TCT	AA	CGG	TGT	GAT
TTT	ACA	TGTC	GTA	GGT	TAT	TTT	TAG	CA	CCT	TAG	TAT	TTCT	GTA	AAA	AGA	TTG	CCC	ACA	CTA
1270					1280			1290				1300			1310			1320	

[illegible]

LYS GLN GLU GLY LYS SER LEU TYR VAL LYS GLY GLU PRO ILE ASN PHE TYR ASP PRO
 AAGCAA GAAGGCAAAAGTCTCTATGTAAAGG TGAA CCAATATAAATTTCTATGACCCCA
 T TCGTTC TTCCGTTTTCAGAGATACATTTTCCCACTTG GTTATTTAAAGATACTGGGT
 1390 1400 1410 1420 1430 1440

[illegible]

GLN SER LEU ALA PHE ILE ARG LYS SER ASP GLU LEU LEU HIS ASN VAL ASN ALA GLY LYS
 CAG AGT TTA GCA TTT A T T C G T A A A T C C G A T G A A T T A T T A C A T A A T G T A A A T G C T G G T A A A
 G T C T C A A A T C G T A A A T A A G C A T T T A G G C T A C T T A A T A A T G T A T T A C A T T T A C G A C C A T T T
 1510 1520 1530 1540 1550 1560

[illegible]

FIG. 5D.

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FIG.	
SY	CLASS
DRAFTSMAN	SUBCLASS

RESTRICTION MAP OF THE RSV F GENE

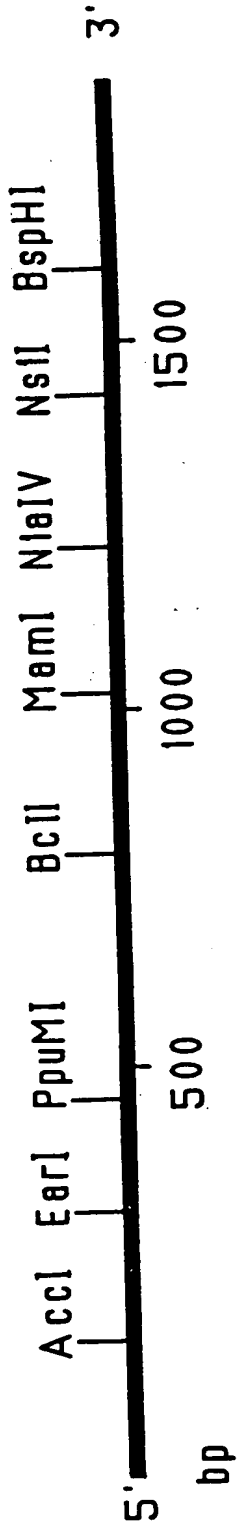


FIG.6.

FIG.7A. NUCLEOTIDE SEQUENCE OF THE RSV G GENE

MET SER LYS ASN LYS ASP GLN ARG
 T G C A A A C A T G T C C A A A A A C A A G G A C C A A C G
 A C G T T T G T A C A G G T T T T T G T T C C T G G T T G C
 10 20 30

THR ALA LYS THR LEU GLU LYS THR TRP ASP
 C A C C G C T A A G A C A C T A G A A A A G A C C T G G G A
 G T G G C G A T T C T G T G A T C T T T T C T G G A C C C T
 40 50 60

THR LEU ASN HIS LEU LEU PHE ILE SER SER
 C A C T C T C A A T C A T T T A T T A T T C A T A T C A T C
 G T G A G A G T T A G T A A A T A A T A A G T A T A G T A G
 70 80 90

GLY LEU TYR LYS LEU ASN LEU LYS SER VAL
 G G G C T T A T A T A A G T T A A A T C T T A A A T C T G T
 C C C G A A T A T A T T C A A T T T A G A A T T T A G A C A
 100 110 120

TM

ALA GLN ILE THR LEU SER ILE LEU ALA MET
 A G C A C A A A T C A C A T T A T C C A T T C T G G C A A T
 T C G T G T T T A G T G T A A T A G G T A A G A C C G T T A
 130 140 150

ILE ILE SER THR SER LEU ILE ILE THR ALA
 G A T A A T C T C A A C T T C A C T T A T A A T T A C A G C
 C T A T T A G A G T T G A A G T G A A T A T T A A T G T C G
 160 170 180

ILE ILE PHE ILE ALA SER ALA ASN HIS LYS
 C A T C A T A T T C A T A G C C T C G G C A A A C C A C A A
 G T A G T A T A A G T A T C G G A G C C G T T T G G T G T T
 190 200 210

VAL THR LEU THR THR ALA ILE ILE GLN ASP
 A G T C A C A C T A A C A A C T G C A A T C A T A C A A G A
 T C A G T G T G A T T G T T G A C G T T A G T A T G T T C T
 220 230 240

ALA THR SER GLN ILE LYS ASN THR THR PRO
 T G C A A C A A G C C A G A T C A A G A A C A C A A C C C C
 A C G T T G T T C G G T C T A G T T C T T G T G T T G G G G
 250 260 270

THR TYR LEU THR GLN ASP PRO GLN LEU GLY
 A A C A T A C C T C A C T C A G G A T C C T C A G C T T G G
 T T G T A T G G A G T G A G T C C T A G G A G T C G A A C C
 280 290 300

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FIG.7B.

ILE SER **PHE** SER ASN **LEU** SER GLU ILE THR
 A A T C A G C T T C T C C A A T C T G T C T G A A A T T A C
 T T A G T C G A A G A G G T T A G A C A G A C T T T A A T G
 310 320 330

SER GLN **THR** THR THR ILE LEU ALA SER THR
 A T C A C A A A C C A C C A C C A T A C T A G C T T C A A C
 T A G T G T T T G G T G G T G G T A T G A T C G A A G T T G
 340 350 360

THR PRO GLY VAL LYS SER **ASN** LEU GLN **PRO**
 A A C A C C A G G A G T C A A G T C A A A C C T G C A A C C
 T T G T G G T C C T C A G T T C A G T T T G G A C G T T G G
 370 380 390

THR THR VAL LYS THR LYS ASN THR THR THR
 C A C A A C A G T C A A G A C T A A A A A C A C A A C A A C
 G T G T T G T C A G T T C T G A T T T T T G T G T T G T T G
 400 410 420

THR GLN THR GLN PRO SER LYS PRO THR THR
 A A C C C A A A C A C A A C C C A G C A A G C C C A C T A C
 T T G G G T T T G T G T T G G G T C G T T C G G G T G A T G
 430 440 450

LYS GLN ARG GLN ASN LYS PRO PRO **ASN** LYS
 A A A A C A A C G C C A A A A C A A A C C A C C A A A C A A
 T T T T G T T G C G G T T T T G T T T G G T G G T T T G T T
 460 470 480

PRO ASN ASN ASP PHE HIS PHE GLU VAL PHE
 A C C C A A T A A T G A T T T T C A C T T C G A A G T G T T
 T G G G T T A T T A C T A A A A G T G A A G C T T C A C A A
 490 500 510

ASN PHE VAL PRO CYS SER ILE CYS SER ASN
 T A A C T T T G T A C C C T G C A G C A T A T G C A G C A A
 A T T G A A A C A T G G G A C G T C G T A T A C G T C G T T
 520 530 540

ASN PRO THR CYS TRP ALA ILE CYS LYS ARG
 C A A T C C A A C C T G C T G G G C T A T C T G C A A A A G
 G T T A G G T T G G A C G A C C C G A T A G A C G T T T T C
 550 560 570

ILE PRO ASN LYS LYS PRO GLY LYS LYS THR
 A A T A C C A A A C A A A A A A C C A G G A A A G A A A A C
 T T A T G G T T T G T T T T T G G T C C T T T C T T T T G
 580 590 600

00473440 010700

FIG.7C.

THR THR LYS PRO THR LYS LYS PRO THR PHE
C A C C A C C A A G C C T A C A A A A A A C C A A C C T T
G T G G T G G T T C G G A T G T T T T T T T G G T T G G A A
610 620 630

LYS THR THR LYS LYS ASP LEU LYS PRO GLN
C A A G A C A A C C A A A A A A G A T C T C A A A C C T C A
G T T C T G T T G G T T T T T T C T A G A G T T T G G A G T
640 650 660

THR THR LYS PRO LYS GLU VAL PRO THR THR
A A C C A C T A A A C C A A A G G A A G T A C C C A C C A C
T T G G T G A T T T G G T T T C C T T C A T G G G T G G T G
670 680 690

LYS PRO THR GLU GLU PRO THR ILE ASN THR
C A A G C C C A C A G A A G A G C C A A C C A T C A A C A C
G T T C G G G T G T C T T C T C G G T T G G T A G T T G T G
700 710 720

THR LYS THR ASN ILE THR THR THR LEU LEU
C A C C A A A A C A A A C A T C A C A A C T A C A C T G C T
G T G G T T T T G T T T G T A G T G T T G A T G T G A C G A
730 740 750

THR ASN ASN THR THR GLY ASN PRO LYS LEU
C A C C A A C A A C A C C A C A G G A A A T C C A A A A C T
G T G G T T G T T G T G G T G T C C T T T A G G T T T T G A
760 770 780

THR SER GLN MET GLU THR PHE HIS SER THR
C A C A A G T C A A A T G G A A A C C T T C C A C T C A A C
G T G T T C A G T T T A C C T T T G G A A G G T G A G T T G
790 800 810

SER SER GLU GLY ASN LEU SER PRO SER GLN
C T C C T C C G A A G G C A A T C T A A G C C C T T C T C A
G A G G A G G C T T C C G T T A G A T T C G G G A A G A G T
820 830 840

VAL SER THR THR SER GLU HIS PRO SER GLN
A G T C T C C A C A A C A T C C G A G C A C C C A T C A C A
T C A G A G G T G T T G T A G G C T C G T G G G T A G T G T
850 860 870

PRO SER SER PRO PRO ASN THR THR ARG GLN
A C C C T C A T C T C C A C C C A A C A C A A C A C G C C A
T G G G A G T A G A G G T G G G T T G T G T T G T G C G G T
880 890 900

05475240-010700

THE **WORLD'S** **GREATEST** **LIBRARY**

NUCLEOTIDE SEQUENCE OF THE RSV G GENE. THE cDNA SEQUENCE IS SHOWN IN THE PLUS (mRNA) STRAND SENSE IN THE 5' TO 3' DIRECTION. THE TRANSMEMBRANE (TM) ANCHOR DOMAIN IS UNDERLINED. AMINO ACIDS DIFFERING FROM THE PUBLISHED PRIMARY SEQUENCE OF THE PROTEIN ENCODED BY THE RSV G GENE ARE BOXED.

FIG. 7D.

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APPROVED	0.6. FIG.
BY	CLASS
DRAFTSMAN	

RESTRICTION MAP OF RSV G GENE

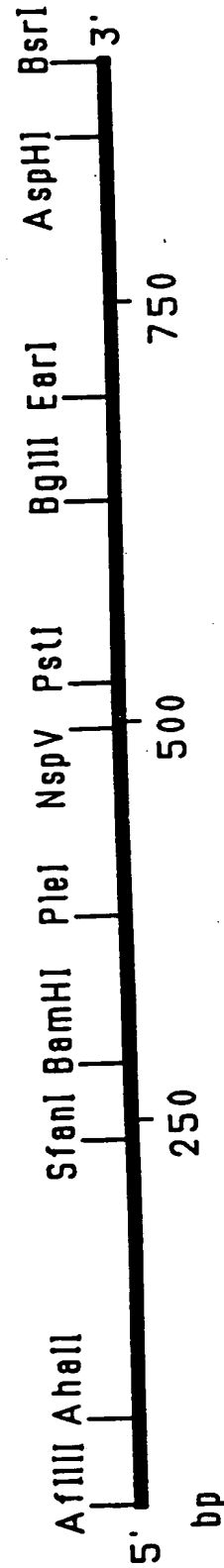


FIG.8.

Construction of a Bluescript-based expression vector containing the chimeric F_{PIV-3}-F_{RSV} gene with the 5' untranslated region of the PIV-3 F gene intact but lacking the nucleotide sequences coding for the hydrophobic anchor domains and cytoplasmic tails of both the PIV-3 and RSV F genes.

Step 1: Preparation of the plasmid containing the modified PIV-3 F gene

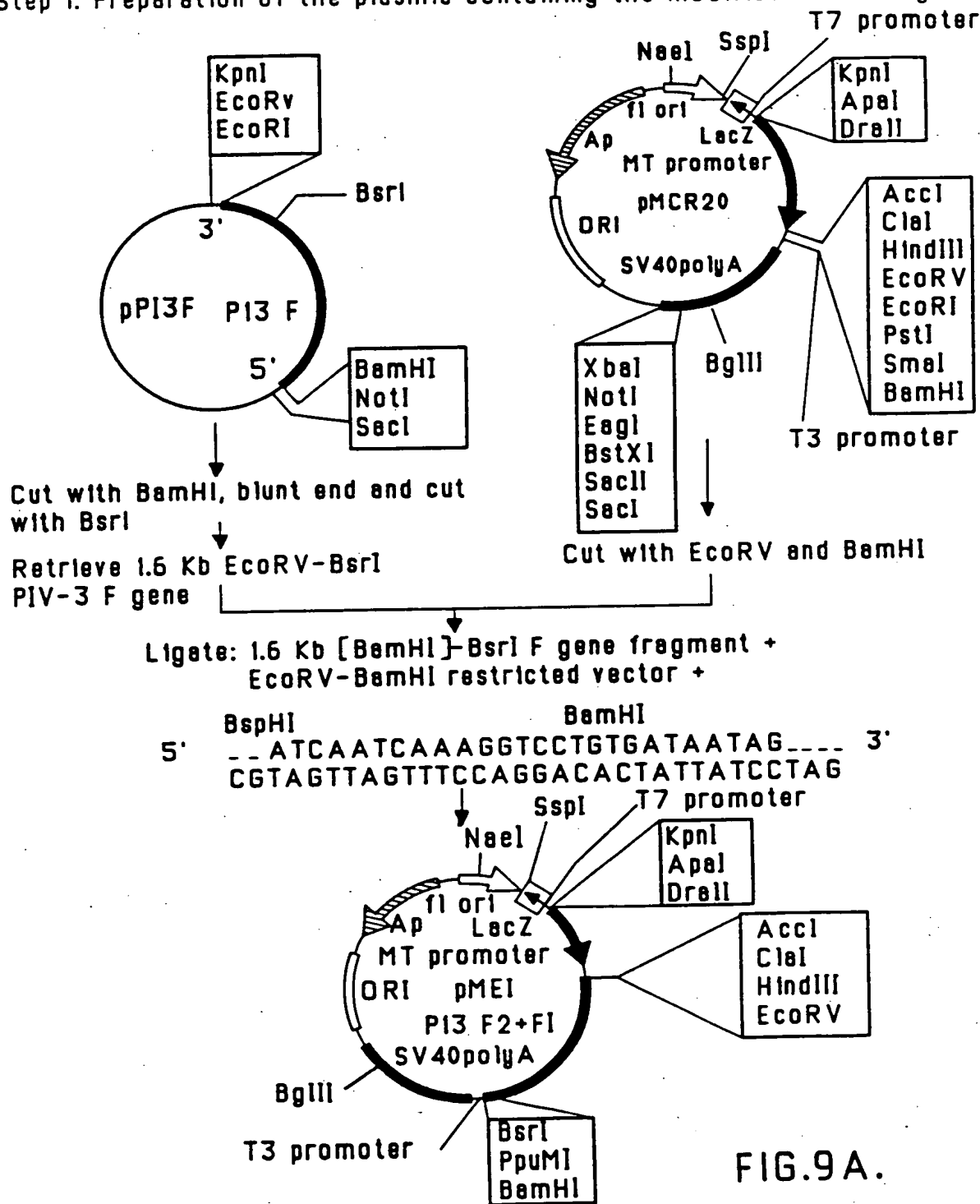
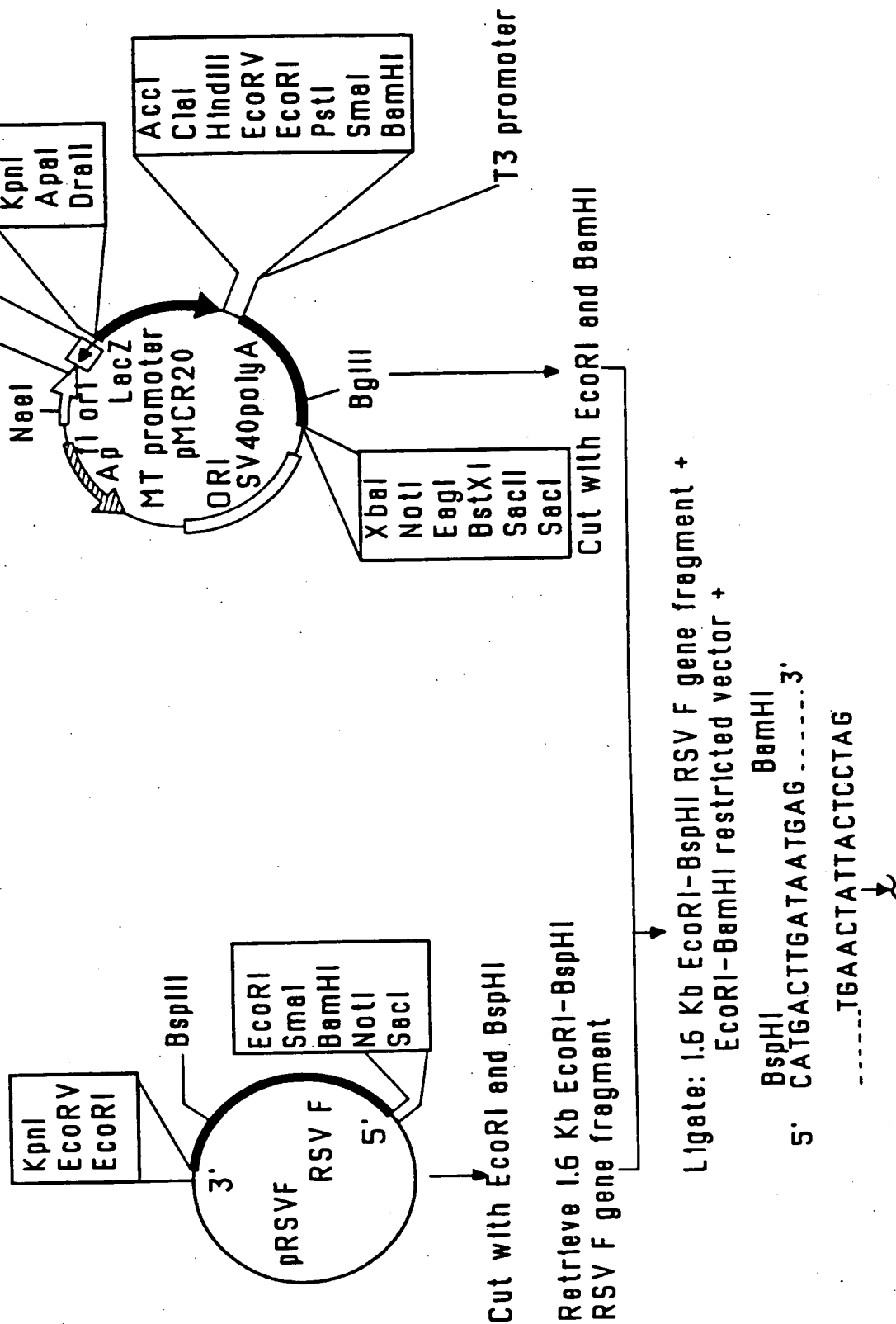


FIG.9A.

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FIG.9B.

Step 2: Preparation of the plasmid containing the modified RSV F gene



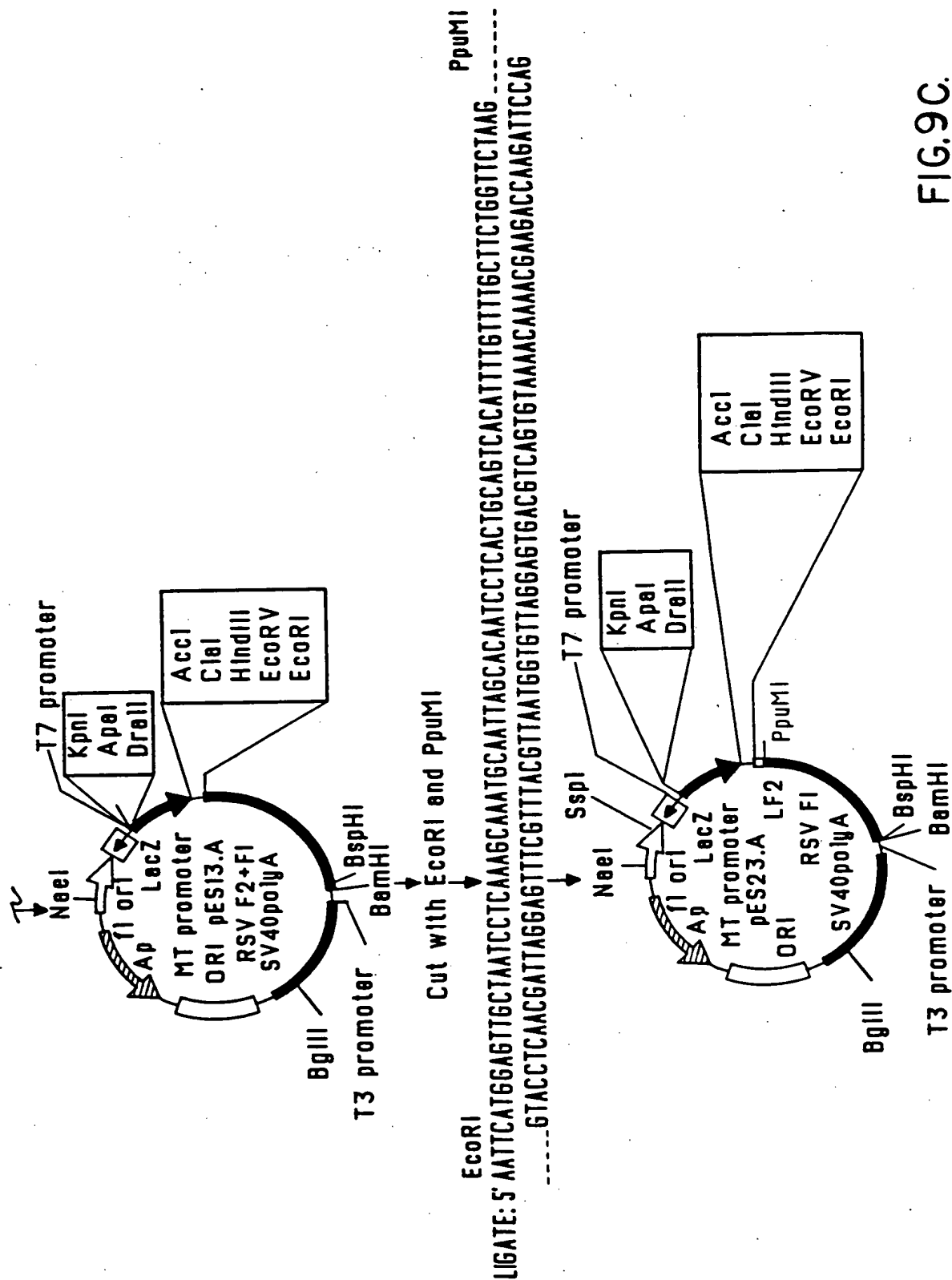


FIG.9C.

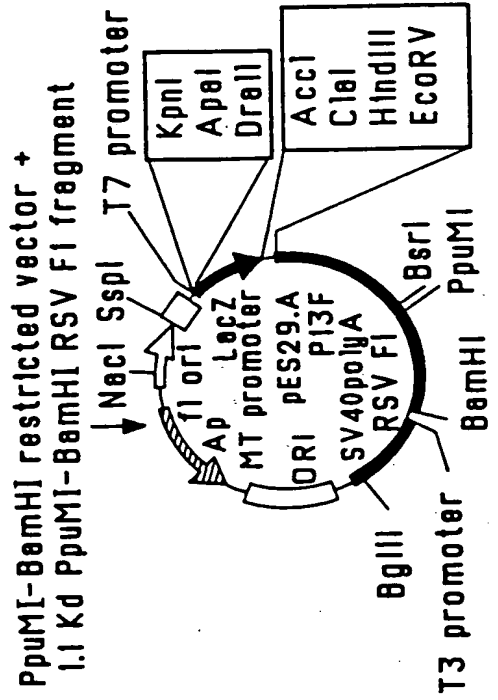
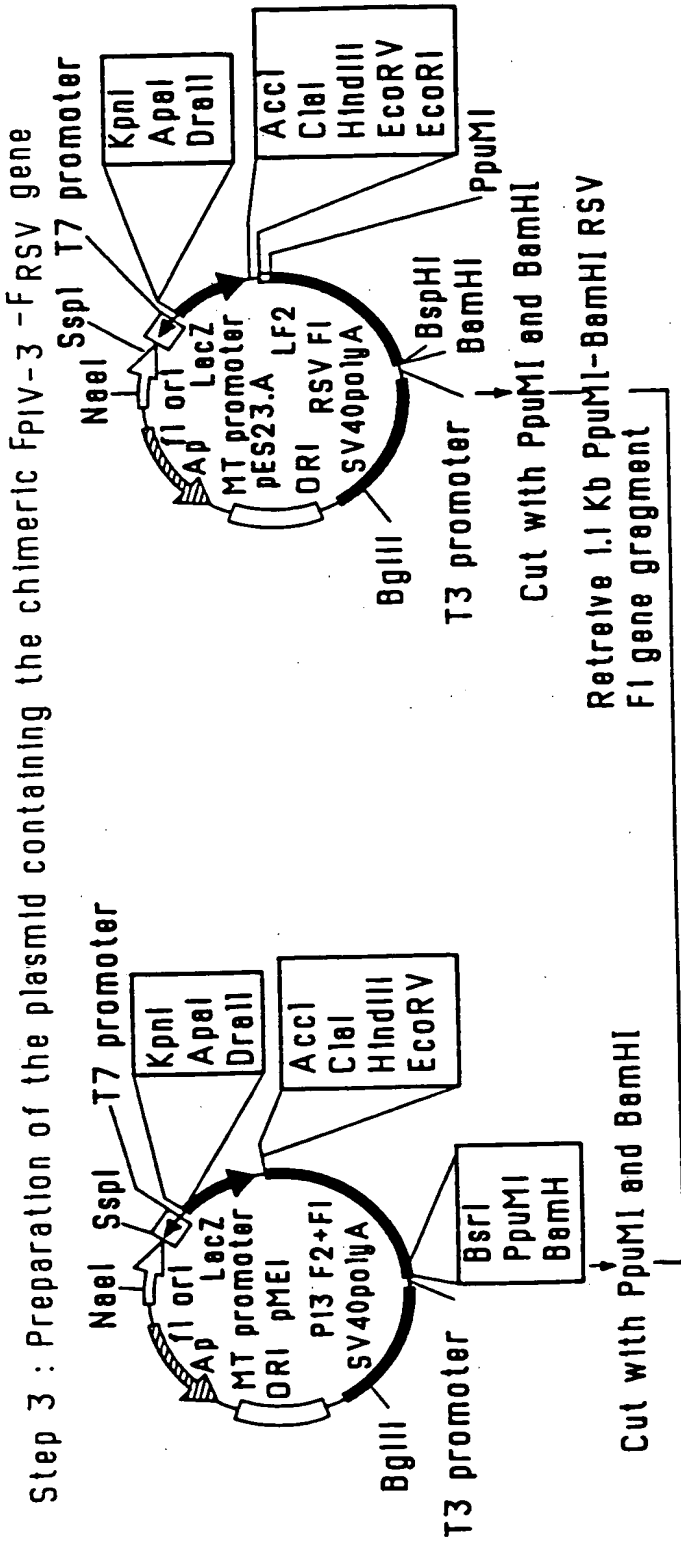


FIG.9D.

Construction of a Bluescript-based expression vector containing the PIV-3 F gene lacking the 5' untranslated sequence and transmembrane anchor and cytoplasmic tail coding regions.

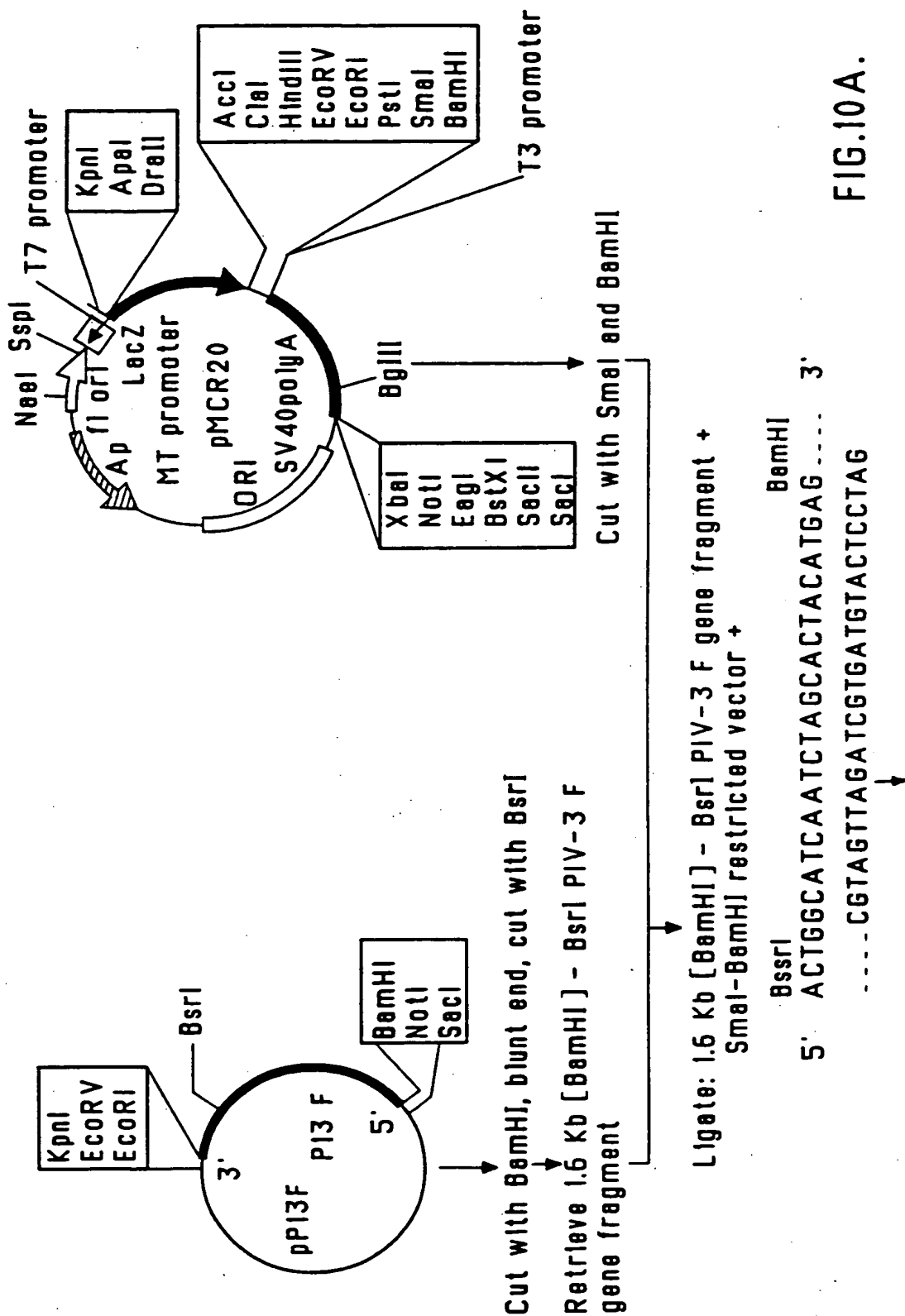
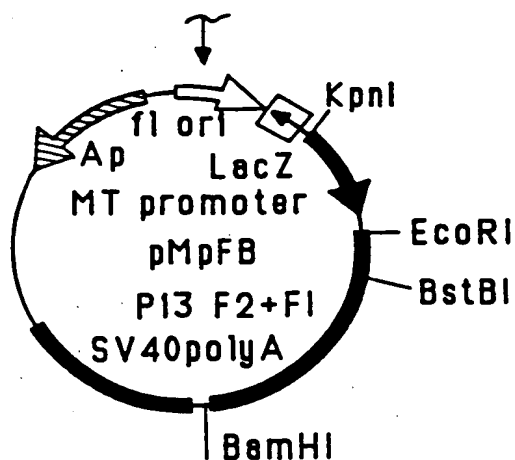


FIG.10A.

FIG.10B.



Cut with EcoRI and BstBI

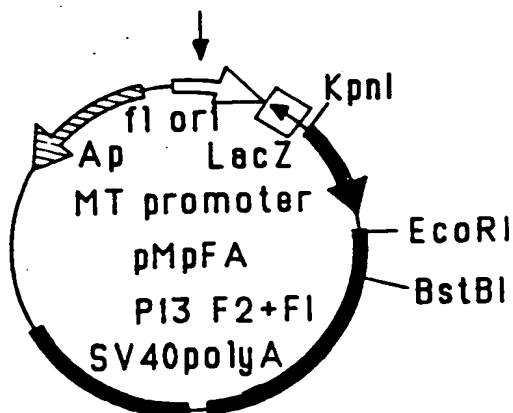
Retrieve: EcoRI-BstBI restricted vector

Ligate: EcoRI-BstBI restricted vector +

EcoRI

PpuMI

AATTCATGCCAACTTTAATACTGCTAATTATTACAACAATGATTATGG
CATCTTCCTGCCAAATAGATATCACAAAACCTACAGCAATGTAGGTGTA
TTGGTCAACAGTCCCAAAGGGATGAAGATATCACAAAACCT 3'
. . . . GTACGGTTGAAATTATGACGATTAATAATGTTGTTACTAATACC
GTAGAAGGACGGTTTATCTATAGTGTTTTGATGTCGTACATCCACATA
ACCAGTTGTCAGGGTTTCCCTACTTCTATAGTGTTTTGAAGCTT



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Construction of the chimeric FPIV-3-FRSV gene consisting of the truncated PIV-3 F gene devoid of the 5' untranslated region linked to the truncated RSV F1 gene.

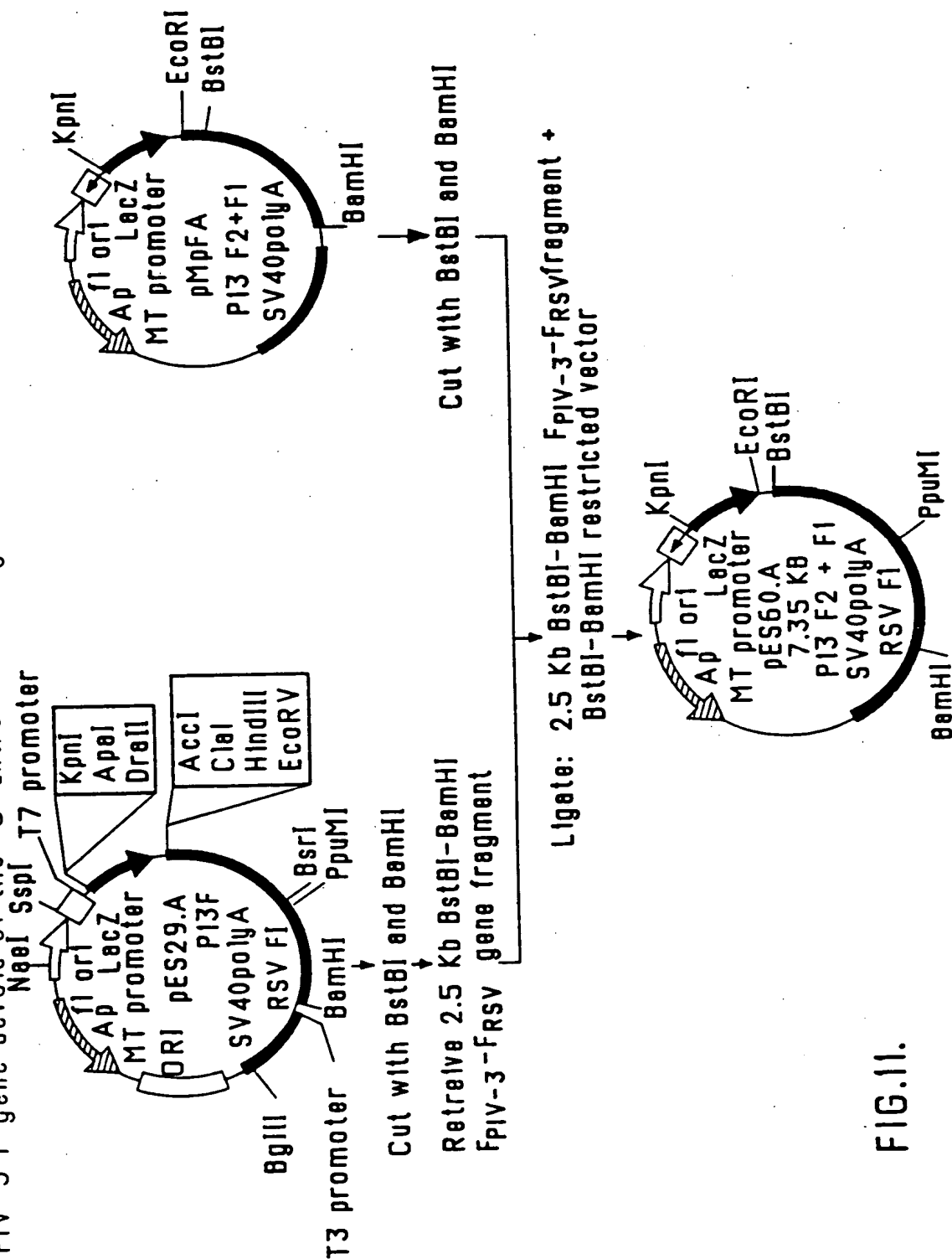
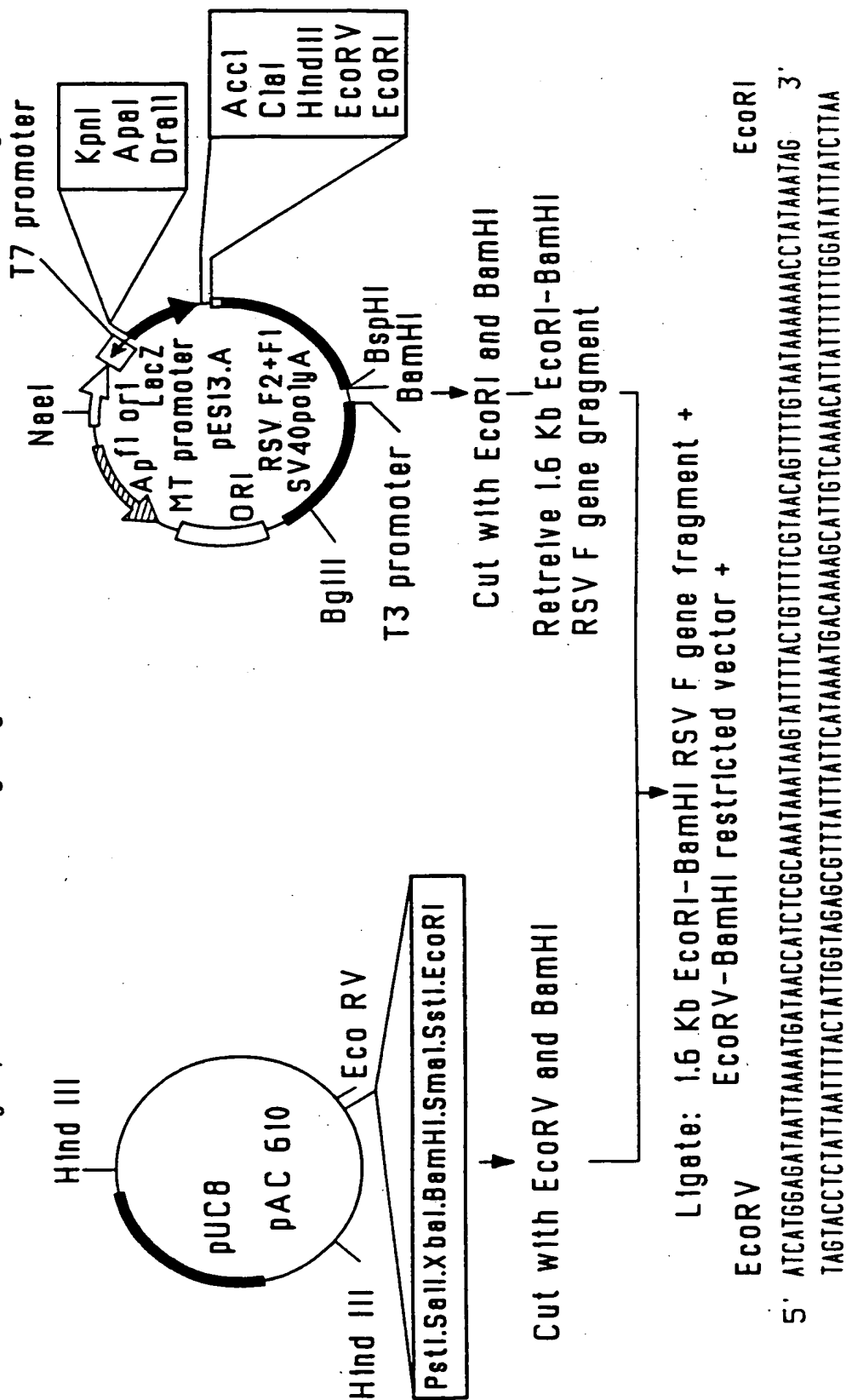


FIG.11.

FIG.12A. Construction of the modified pAc 610 baculovirus expression vector containing the chimeric Fpiv-3-FRSV gene consisting of the PIV-3 F gene lacking both the 5' untranslated sequence as well as the transmembrane and cytoplasmic tail coding regions linked to the truncated RSV F1 gene



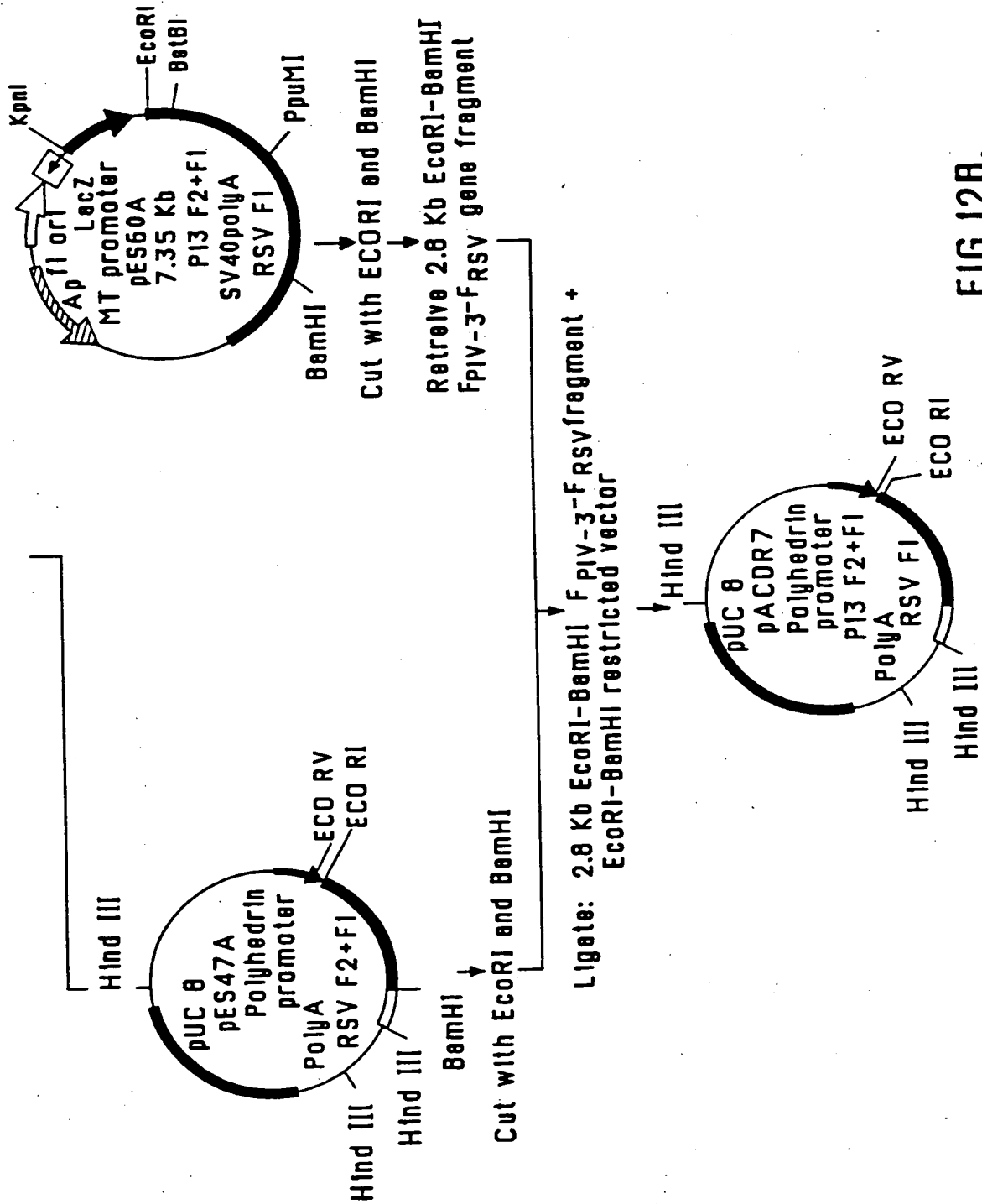


FIG.12B.

FIG.13

**IMMUNOBLOTS OF CELL LYSATES FROM Sf9 CELLS
INFECTED WITH RECOMBINANT BACULOVIRUSES**

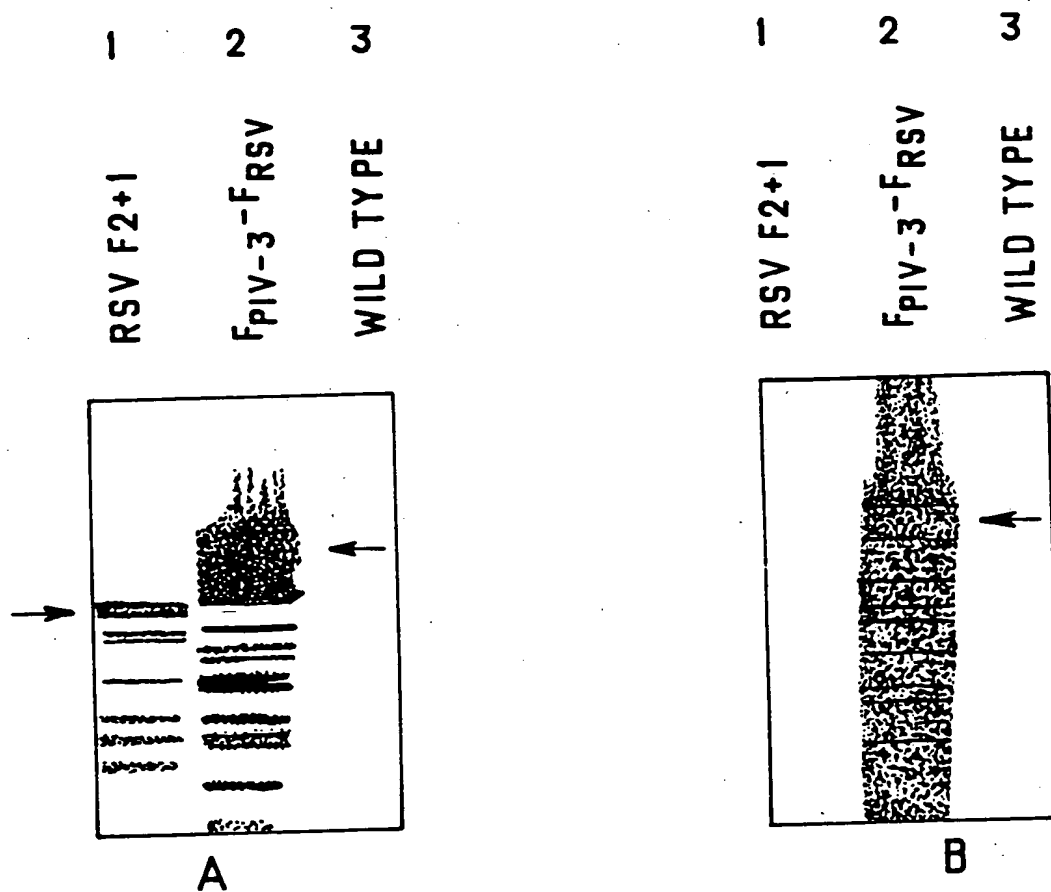
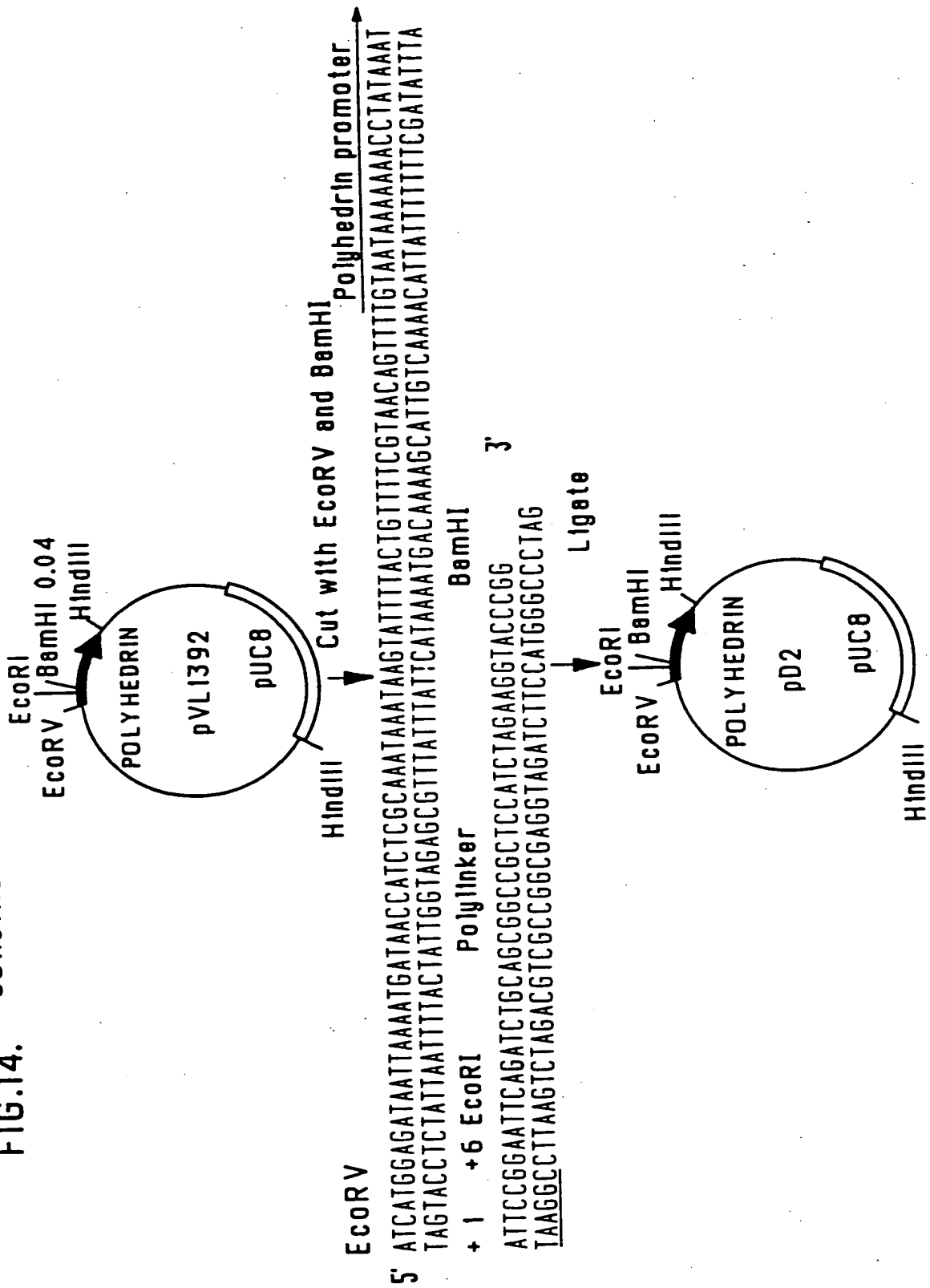


FIG 13 : Immunoblots of cell lysates from Sf9 cells infected with recombinant baculoviruses containing the truncated RSV F gene (Lane 1), the chimeric FPIV-3-F RSV gene (Lane 2) or infected with wild type virus (Lane 3) reacted with anti-F RSV Mab (panel A) and anti-F1 PIV-3 antiserum (panel B)

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FIG. 14.



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FIG.15A. CONSTRUCTION OF THE $F_{RSV-HNPIV3}$ CHIMERIC GENE

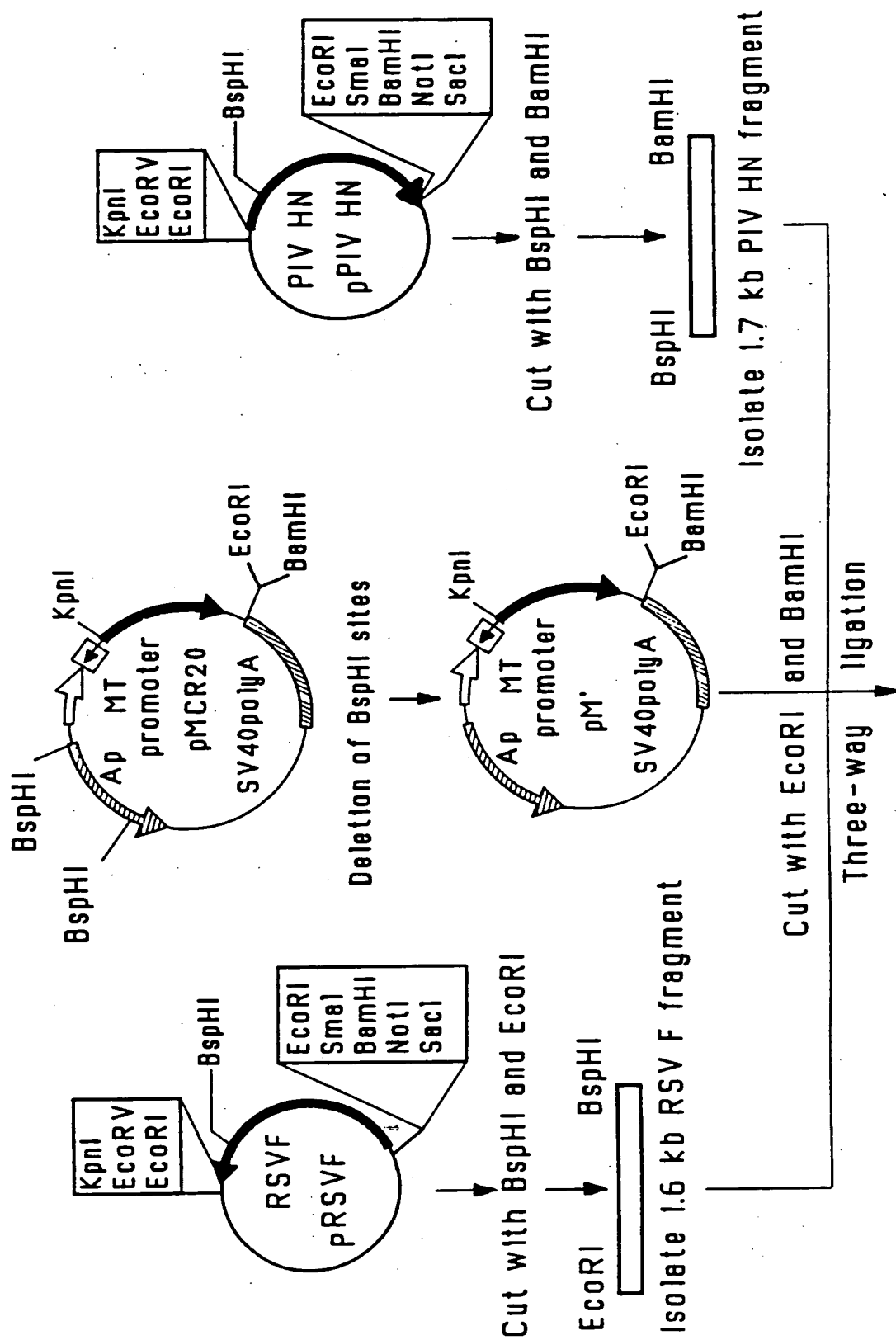
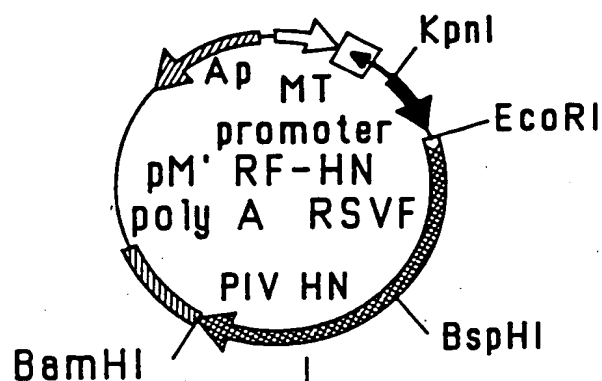


FIG.15B.

THREE-WAY LIGATION



Cut with BspHI

5' ^{BspHI} CATGACTAATTCCATCAAAAGTGAAAAGGCT ^{BspHI} 3'
 TGATTAAGGTAGTTTTCACTTTTCCGAGTAC

Ligation of BspHI-BspHI linker

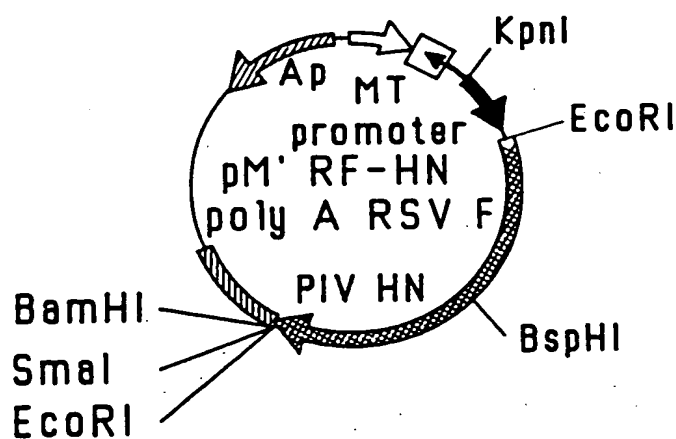


FIG.16

SDS POLY ACRYLAMIDE GEL AND IMMUNOBLOTS OF
PURIFIED F_{RSV}-HN_{PIV-3} CHIMERIC PROTEIN

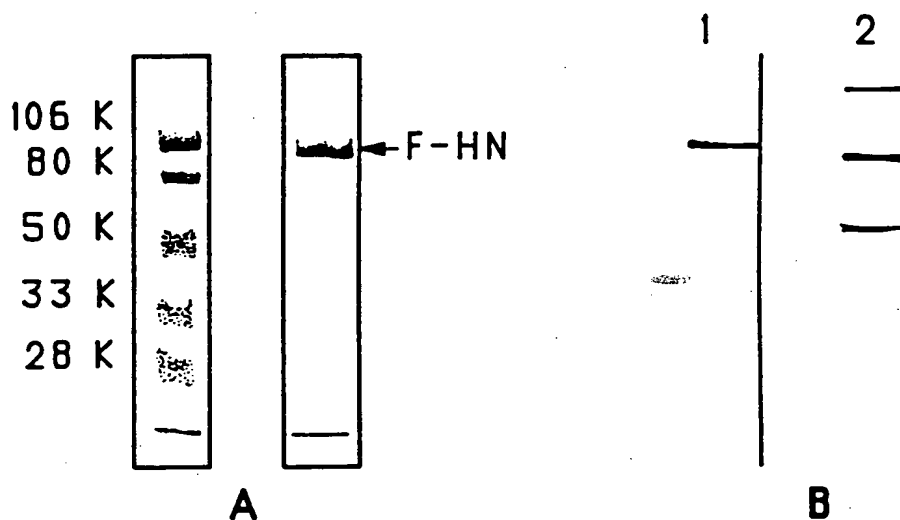
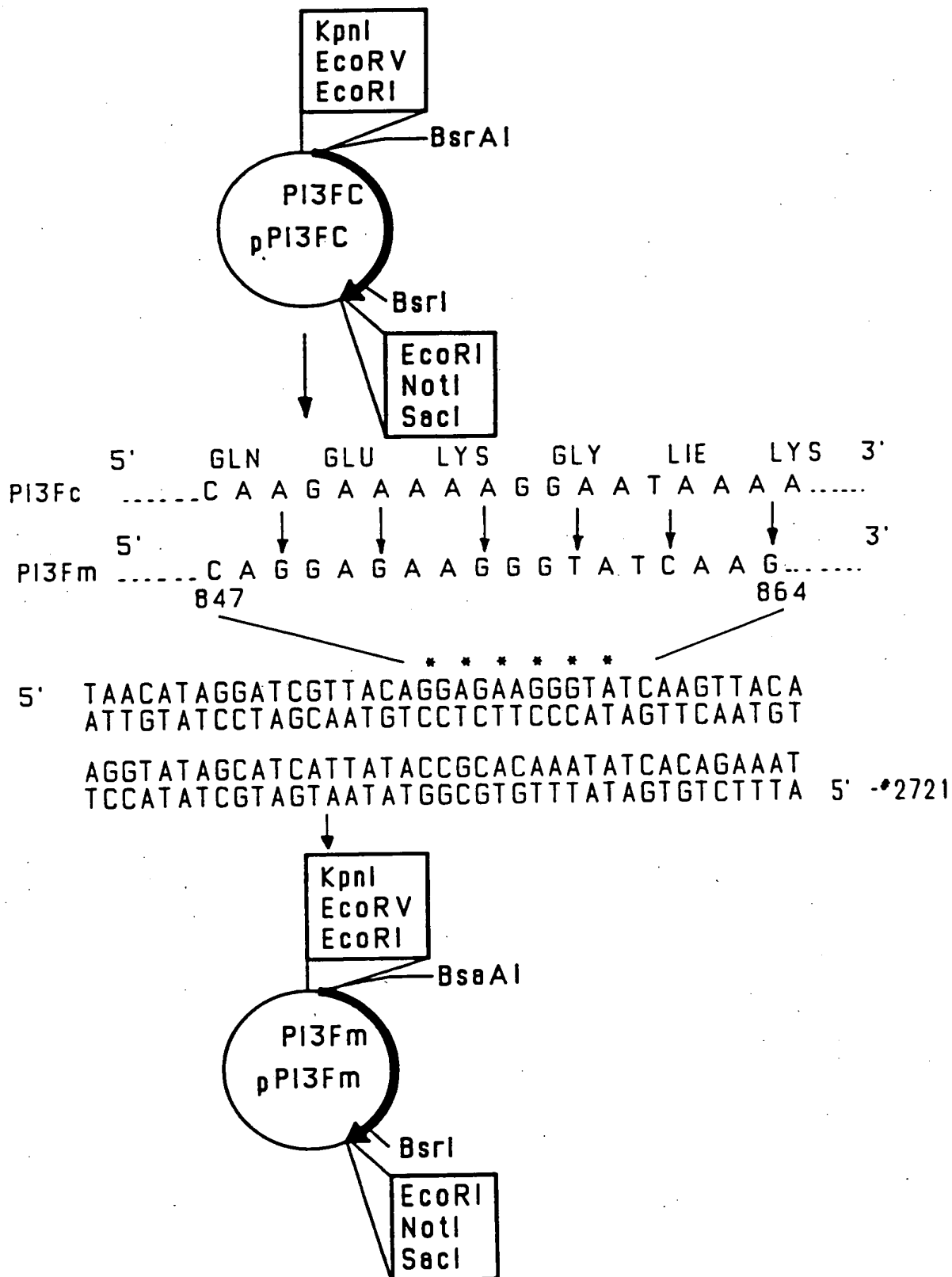


FIG 16 : A) Coomassie-stained SDS polyacrylamide gel of immunoaffinity- purified F_{RSV}-HN_{PIV-3}protein.

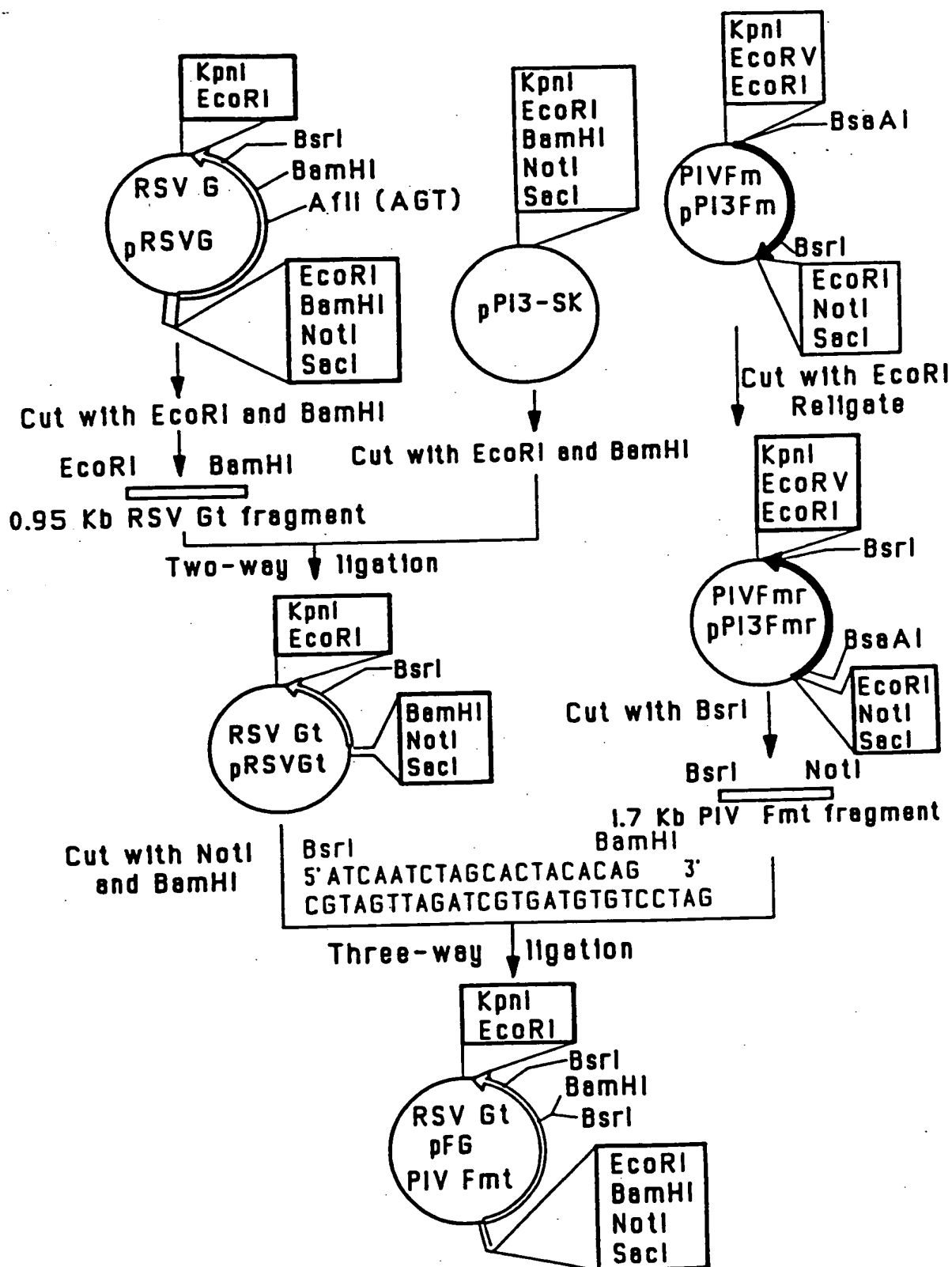
B) Immunoblots of F_{RSV}-HN_{PIV-3}protein reacted with an anti-F RSV Mab (lane 1) and anti-HN PIV-3 antiserum (lane 2)

FIG.17. MUTAGENESIS OF THE PIV-3 F GENE



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FIG.18. CONSTRUCTION OF THE F_{PIV3}-G_{RSV} CHIMERIC GENE



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